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Search information block:
Query: US-09-488-265-25
Query length: 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                         score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search time (sec): 54.640000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database sequences: 231628
Database length: 24425594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MODEL=frame+_n2p.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09488265/runat_03072002_091241_4286/app_query.fasta_1.4477
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai
-GAPOP=12.000 -GAPEXT=4.000 -MINKATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPDP=4.500 -GGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=PCt -THR_MAX=100 -THR_MINCH=15 -MODE=LOCAL
-OUTPMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US09488265_@CGN1_1_67 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
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      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                 84
               eTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgA
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; OTHER INFORMATION: Description of Artificial Sequence:consensus; OTHER INFORMATION: sequence US-09-121-425-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09121425 Patent_No. 6153418
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ORGANISM: Artificial Sequence
440 CTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAG
                                                                                                                                                                                                                                                                                                                                                    340 AGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACCTTTGGGTGCTGAC
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Ratio: 5.093
milarity: 97.279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheGlnSerAlaLysLeuAlaAspProGlySerGlnProHisGlnAlaSe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCCAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCCACCACCAAGCTTC 589
gCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyG
                                                                                                                                                                 luMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheS
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1390 GTAACTGGGAAGAATGTTTCGCT 1412

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-09-121-425-2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09121425 Patent No. 6153418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: 05/09/121,425
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
FILE REFERENCE: consensus phytases 13239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 467
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 lyAsnTrpAlaGluCysPheAla 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
                                         412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
                                                                                                                                                                                                                      312
                                                                                                                                                                                                                                                                                                                                                                                               212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 rSerGlyThrAlaLeuGlyProArgGlyAsnSerHisSerCysAspThrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerTh 17
.ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluA 114
                                                                                                                               GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
                                                                                                                                                                                                                    GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 363
                                                                                                                                                                                                                                                             laArgTyrProThrSerSerLysSerLysAlaTyrSerAla......
                                                                                                                                                                                                                                                                                                                                               TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 2173.00
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89.322
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1252 GTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTTGGTTAACGACAGAGAGTT 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1002 CCAGTTCAAGACCACACTTCTACCTAAGCACACTTTGGACTCTAAGCCAGC 1051
                                                                                                397 aSerTrpThrValProPheGlyAlaArgAlaTyrValGluMetMetGlnC 414
                                                                                                                                                                                                                                                                                              364 erMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
414 ysGlnAlaGluLysGluProLeuValArgValLeuValAsnAspArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 ProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnProAl 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 laGlnGlyValGlyPheAlaAsnGluLeuIleAlaArgLeuThrArgSer 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              902 ATCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAG 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCA 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 ysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            802 GTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 PheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAspLe 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 TTCACTGCTGTTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTT 751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652 TGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAAC 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 sValIleIleProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLy 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCCAGTTATTAAC...... 602
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                                                                                                                       TTCTTGGACTGTTCCATTCGCTGCTACAGCTTACGTTGAAATGATGCAAT 1251
                                                                                                                                                                                                                                                                                                                                                                                              aThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nSerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTATTATTCCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTT 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaA 164
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seq_documentation_block:
    Sequence 33, Applicati
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Ca
TELECOMMUNICATION INFORMATION:
TELECHONE: (201) 235-4205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1402 AATGTTTCGCT 1412
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                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PO NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                              FEATURE:
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van Loon, APPLICANT: Mitchell,
                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 luCysPheAla 467
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                                                                                                                  OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                               NAME/KEY: misc_feature LOCATION: 205
                                                                                                                                                                                          OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 104
OTHER INFORMATION: /note="potential N-glycosylation site"
                                           OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 119
LOCATION:
                 NAME/KEY:
                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 340 |
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/868,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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6291221
                                                                                                                                                                                                                                                                                                                                                                                     amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
 misc_feature
337
                                                                                                                                                                                                                                                                                                                                                                         Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adolphus
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; NAME/KEY: misc_feature
; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-868-435-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-488-265-25 x US-08-868-435-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
                                       662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 alAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeuTrpGlyGln 49
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spProGlyAlaThr...AsnArgAlaAlaProAlaIleSerValIleIle
                                                                                                                                                                                                                                                          eAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaA 183
                                                                                                                                                                                                                                                                                                TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
                                                                                                                                                                                                                                                                                                                                            AlaargSerValValProPheIleArgAlaSerGlySerAspArgValIl 166
                                                                                                                                                                                                                                                                                                                                                                                  GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
                                                                                                                                                                                                                                                                                                                                                                                                                            AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
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                                                                                                                         CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
                                                                                                                                                                                                                  ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-33
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                                                                                                                                                                                                                                               1262 AAAGGAACCATTGGTTAGAGTTTTGGGTTAACGACAGAGATTGTTCCATTGC 1311
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                                                                                            1412 T 1412
                                                                                                                                232 euPheAlaProAspIleArgAlaArgAlaGluLysHisLeuProGlyVal 248
                                                                                                                                                                                                                                                                                                                                                                                                           382 hrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIl
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seq\_documentation\_block:

Sequence 33, Application US/08744231

GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc

Patent No. 6358722

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alignment_block:
                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-744-231-33
                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                Align sey 1/1 to: US-08-744-231-33 from: 1 to: 465
                                                                                                                                                                           US-09-488-265-25 x US-08-744-231-33
                                                                                                                                                                                                                                        Percent Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
            62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
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APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
                                                 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyAr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note="potential N-glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
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REGISTRATION NUMBER: 32142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/744,231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Nutley
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Ratio: 4.507
milarity: 90.364
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                                                                                                                                                                                                                               Percent Identity: 77.088
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Length:
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912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGGTCAAGGTGT 961
                                                                                                                                                                                                                                                                                                            812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
                                                                                          299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIl 315
                                                                                                                                                                                     282 euPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 laArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 TyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLe 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 alAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeuTrpGlyGln 49
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                                                                                                                                                                                                                                                                                     \tt pThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnL
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 8, Application US/07923724
Patent No. 5780292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1062 TIGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 hrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 rIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 LeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSe 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432 isGlyCysAspValAspLysLeuGlyArgCysLysLeuAsnAspPheVal 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 uLysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuH 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 LysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSe 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 r 465
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Turunen, Marja K.

APPLICANT: Fagerstr m, Richard B.

TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                     APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          STATE: D.C.
                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                       STREET:
APPLICATION NUMBER: US 07/496,155
                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                            E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miettinen-Oinonen, Arja S.K.
Torkkeli, Tuula K.
Cantrell, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nevalainen, Helena K.M.
Paloheimo, Marja T.
                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rambosek, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piddington, Christopher S.
                                                                                                                                   PatentIn Release #1.0, Version #1.25
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US-07-923-724-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-488-265-25 x US-07-923-724-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 89.722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 3/1-2540 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 29-APR-1987 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
                                                                                                                                                                                                                                             312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
                                                                                                                                                                                                                                                                                                                                                            212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150
                                                                                                                      412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
                                                                                                                                                              117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG
                                                                                                                                                                                                   362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
                                         462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
                                                                                                                                                                                                                                                                                                                        67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/044,077 FILING DATE: 29-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Cimbala, Miche REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-MAR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 1866.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467 amino acids
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1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGATACTGGGAAGAATGTTTCGC 1411
                                                                                                                                                      1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
                                                                                                                                                                                                                                  1262 AAAGGAACCATTGGTTAGACTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
                                                                                                                                                                                                                                                                                                                                        1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
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451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467
                                                                                                   434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
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                                                                                                                                                                                                         417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
                                                                                                                                                                                                                                                                                                          401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417
                                                                                                                                                                                                                                                                                                                                                                                                           384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300
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alignment_block:
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                                                                                                         alignment_scores:
US-09-488-265-25 x US-08-609-426A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-8
                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5830733 GENERAL INFORMATION:
                                                                                                                                                                                                                                               TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 105
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                          LENGTH: 467 amino acid
                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 29-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08
FILING DATE: 01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20005
                                                                          Ratio:
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                                                                                                                                                                                                                           467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piddington, Christopher S. Rambosek, John A. Turunen, Marja K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fagerstr m, Richard B.
                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nevalainen, Helena K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sterne, Kessler, Goldstein & Fox
                                                     4.453
89.722
                                                                                       1866.00
                                                                                                                                                                              protein
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                                                     Percent Identity:
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                                                                                     Length:
                                                     74.518
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Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167
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                                                                                                                                                                                                                                                                                                                                                                                 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC
                                                                                                                                                                                                                            762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
                                                                                                                                                                                                                                                                                                                                                                                 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
                                                                           pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL
                                                                                                                                                                          {\tt ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs}
                                                                                                                                                                                                                                                                             hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250
                                                                                                                                                                                                                                                                                                                             TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150
                                                                                                                           CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
                                                                                                                                                                                                                            AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-652C-2
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application patent No. 5834286 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467
                                                                                                                                                             APPLICANT: HOUSTON, CHRISTINE S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: APPLICANT:
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                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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               COUNTRY:
                                       STATE:
                                                         CITY: WASHINGTON
                                                                               STREET:
                                                                                                   ADDRESSEE:
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20005
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                                                                           EE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                   USA
                                                                                                                                                                                                                                                                          TURUNEN, MARJA K.
RAMBOSEK, JOHN A.
PIDDINGTON, CHRISTOPHER S.
                                                                                                                                                                                                                                                   HOUSTON, CHRISTINE S.
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                                                                                                                                                                                                                                                                                                                                                            PALOHEIMO, MARJA T. FAGERSTROM, RICHARD B.
                                                                                                                                                                                                                                                                                                                                                                                                      NEVALAINEN,
                                                                                                                                                ENZYMES IN DESIRED RATIOS 94
                                                                                                                                                                                                                                                                                                                                                                                                        HELENA K.M.
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COMPUTER READABLE FORM:

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alignment_scores:
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NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1050,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEPAX: 202-371-2540
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
                                                                                                 312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
                                                         162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
                                                                                                                                                                                                                                                                                                                                                                                                           112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-UUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                       51 TyrAlaProPhePheSerLeuAlaAsnGluSerAlaIleSerProAspVa 67
                                                                                                                                                                                                                                                                                                                                                                                   34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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Ratio: 4.453
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| 417<br>131<br>434 | O1 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaG1  62 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC   ::: | 12 4     |
|-------------------|--|----------|
| , N               | 112 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA   | 12       |
| 121<br>400        | 62 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT  | 3        |
| 116<br>384        | 12 TATTITCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA  | 11<br>3  |
| 111<br>367        | 062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC   | =        |
| 106<br>350        | 012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA<br>   | <u>-</u> |
| 10                | 962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG<br>    :::::  |          |
| 96<br>31          | 912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT<br>           :::   |          |
| 91<br>30          | 862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT   |          |
| 28                | 812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT     :::::::::::::::::::::::::::::    ::::                   |          |
| 81<br>26          | 762 AACTTGACTGACGAAGACGTTGTTGTTGATTGGACATGTGTCCATTCGA :::  |          |
| 76<br>25          | 712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT ::  |          |
| 71<br>23          | 662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG   |          |
| 66<br>21          | 612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC   |          |
| 61<br>20          | 562 ACCCAGGTGCTAACCCACACCAACCTTCTCCAGTTATTAACGTTATTATT   |          |
| 18<br>18          | 512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG        :::  |          |
| 51<br>16          |  |          |
| 15                | 412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG   ::::::  |          |
| 13                | 117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG   |          |

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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-151-574-32
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                                                  alignment_block:
                                                                                                                                       alignment_scores:
                                                                                                                                                                                         ; MOLECULE TYPE: US-08-151-574-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32, Patent No. 5
                                 US-09-488-265-25 x US-08-151-574-32
                                                                                     Percent Similarity:
Align seg 1/1 to: US-08-151-574-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1412 T 1412
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ## 151 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysSerAl 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Cloning TITLE OF INVENTION: Phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rudolf G.M. Luttin APPLICANT: Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 a 467
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 24-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Morrison & Foerster
Mr: 545 Middlefield Road, Suite 200
Menlo Park
                                                                                                                        Quality: 1862.00
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                                                                                                                                                                                                                                             amino acid
                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
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                                                                                                                                                                                                                                                                 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                               amino acids
                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: 07/688,578
24-MAY-1991
                                                                                     4.433
89.936
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                                                                                                                                                                                                                                                                                                     32:
                                                                                       Percent Identity:
                                                                                                                                                                                                                                                                                                                                                       24615-20026.00
 from: 1
                                                                                                                      Length:
 to: 467
                                                                                     74.518
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112 TTGACGGTGGTTACCAATGTTTCCCCAGAAATTTCTCACTTGTGGGGTCAA 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 TACTCTCCATTCTTCTCTTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 CTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGAATTGAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
                                                                                                                                                                                                                                                                                                                                                                                                 712 TTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
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                                                                                                                                                                                                   812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
                                                                                                                                                                                                                                                                             234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa
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912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
                                                                                                 862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
                                                                                                                                                                                                                                                       251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217
                                               euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
                                                                                                                                                 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/08146424 Patent No. 5593963 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              APPLICANT: VAN OULLEN,
APPLICANT: VAN OULLEN,
APPLICANT: RIETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
APPLICANT: TOVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,424
FILING DATE: 02-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGGAAGAATGTTTCGC 1411
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CTREET: 755 Page Mill Road
                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                  COUNTRY:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
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                                                                                                                                                                                               94304-1018
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alignment_scores:
Ouality: 1862.00
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TELEX: 706141
TELEX: 706141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
FUNGTH: 467 amino acids
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167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184
                                                                                          512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG
                                                                                                                                                                                                                                               134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu
                                                                                                                                                                                                                                                                         412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
                                                                                                                                                              151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl
                                                                                                                                                                                                         462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
                                                                                                                                                                                                                                                                                                                                         117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 44615-20011.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 467 amino
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC
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REGISTRATION NUMBER: 33,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
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Percent Identity: 74.518
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1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
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                                        1412 T 1412
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467 a 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                           hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATTITCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCAITGTCTACTA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334
                                                                                                                                                                                                                                                  uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-693-709-2
seq_documentation_block:
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; NAME/KEY: Signal Sequence; LOCATION: 1...23; OTHER INFORMATION: US-08-693-709-2
                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08693709 Patent No. 5770413 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                              Align seg 1/1 to: US-08-693-709-2 from: 1 to:
                                                                                                                                                                                                                  US-09-488-265-25 x US-08-693-709-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SIJMONS, I APPLICANT: VERWOERD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NUMME: MUTAShige, Kate H
REGISTRATION NUMBER: 29,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: US APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800 PRIOR APPLICATION DATA:
112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                               17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34
                                                                   62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
                                                                                                                                            12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MURALLO ROAD
                                                                                                       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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HOEKEMA, ANDREAS
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Percent Identity: 74.518
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1012 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1061
                                                                     962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 101:
                                                                                                                                                                                      912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 961
                                                                                                                                                                                                                                                         284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
                                                                                                                                                                                                                                                                                                        862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
                                                                                                                                                                                                                                                                                                                                                                                                   812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
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200
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seq_documentation_block:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 32:
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                                                                                     FILING DATE: 10-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTASTIGE, Kate H.
REGISTRATION NUMBER: 29,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
                                                                                                                                                                                                            CURRENT APPLICATION DATA: US.
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 a 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2000 Peni
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20006-1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Annemarie E. Veenstra
Rudolf G.M. Luttin
Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert F.M. Van Gorcom
Willem Van Hartingsveldt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petrus A. Van Paridon
                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytase
: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and Expression of Microbial
                                                                                                                                                                                                               US/08/419,448
                                                                                           29,959
                                                                    24615-20026.10
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; MOLECULE TYPE: protein US-08-419-448-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-419-448-32 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-488-265-25 x US-08-419-448-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                             151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         662 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 467 amino TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34
TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
                                                                                                       SerGluAlaSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217
                                                                                                                                                                 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 661
                                                                                                                                                                                                                                                                               ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
                                                                                                                                                                                                                                                                                                                                  eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 1862.00
Ratio: 4.433
milarity: 89.936
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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-3
                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                      Sequence 3, Application US/08819825 Patent No. 5866118
                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1312 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1262 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1162 CTTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1112 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1062 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1111
APPLICANT: Berka, Randy M.
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NITMERR OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                  1412 T 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1362 GAAGGTTTGTCTTTCGCTAGATCTGGTGAACTGGGAAGAATGTTTCGC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 rileLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL
                                                                                                                                                                                                                                                                                                                                                                 467 a 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ### 151 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
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alignment_block:
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Ratio: 4.433
Percent Similarity: 89.936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-819-825-3 from: 1 to: 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212 867 0123
TELEPHONE: 212 867 0123
TELEPAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117
                                                                                   312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
                                                                                                                               162 TACTCTCCATTCTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
                                                                                                                                                                                                                                                                                                                                                       112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                    51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67
                                                                                                                                                                                                                                                                                                                                   34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50
                                                                                                                                                                                                                                                                                                                                                                                                     62 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/819,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TE: New York VTRY: U.S.A. 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAR-1997
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Gaps: 0
Percent Identity: 74.518
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| 131<br>434 | FCCATTGC  | 1262<br>417 |
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| 126<br>417 | GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA<br>           :::                                | 1212<br>401 |
| 121<br>400 | CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT<br>  :::      :::  <br>                          | 1162<br>384 |
| 116<br>384 | TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA  | 1112<br>367 |
| 111<br>367 | TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC  | 1062<br>351 |
| 106<br>350 | ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA  | 1012        |
| 101<br>334 | TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG<br>    :::::                                     | 962<br>317  |
| 961<br>317 | AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT            :::                                   | 912<br>301  |
| 91]<br>30( | TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT<br>  | 862<br>284  |
| 86:        | CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGAGATTGTGTAGACT                                       | 812<br>267  |
| 81:<br>26  | AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA:::   | 762<br>251  |
| 76:<br>25! | TTTTCGCTCC::  ::  <br>::   ::: <br>hrPheValP;   | 712<br>234  |
| 71<br>23   | TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG:   | 662<br>217  |
| 66<br>21   | CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC  | 612<br>201  |
| 61<br>20   | 10 — 7  |             |
| 56<br>18   | 2 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG<br>       :::::                    :::         | 512<br>167  |
| 51<br>16   | 2 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGATTAT :::   :::                                     | 462<br>151  |
| 46<br>15   | <pre>2 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG   :::::                            </pre> | 412<br>134  |

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seq_documentation_block:
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                                                                                                                                                                                                                                                                      US-09-163-642-3
                                                                                                                        alignment_block:
                                                                                                                                                                                                                alignment_scores:
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                                                                                                         US-09-488-265-25 x US-09-163-642-3
                                                                     Align seg 1/1 to: US-09-163-642-3
                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 a 467
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                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                               12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 405 Lexi
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/163,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                               Quality: 1862.00
                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                               212 867 0298
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89.936
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Percent Identity: 74.518
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101 GluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
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                                                                                                                                                                                                                                                                         812 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 861
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                                                                                                                                                                                                                                                                                                                                                                                                                                               234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234
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962 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1011
                                                                                                                                                                                                                                                                                                                                                                                                762 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 811
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                                                                        AAGTACTACGGTTACGGTGCTAGTAACCCATTGGGTCCAGCTCAAGGTGT 961
                                                                                                                                                 euPheThrHisaspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
                                                                                                                                                                                             TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
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                                              LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa
                                                                                                                                                                                                                                            pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284
                                                                                                                                                                                                                                                                                                                                                    ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267
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seq_documentation_block:
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                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 a 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367
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                                                                                                                                                                                                                                                                                                                                                   STREET: 545 Midd
CITY: Menlo Park
STATE: Californi
                                                    CLASSIFICATION:
                                                                                 FILING DATE:
                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                  94025-3471
                                                                                                                                                                                                                                                                                                                                              California
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                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
07/688,578
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alignment_block:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acid
                                                                                                                                                                                                               562 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
                                                     167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184
                                                                                                                                                                        462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
                                                                                              512 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 561
                                                                                                                                    151 ThrargasnIleValProPheIleArgSerSerGlySerSerArgValIl 167
                                                                                                                                                                                                                                                                                                362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC
                                                                                                                                                                                                                                                                                                                                                                             101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117
                                                                                                                                                                                                                                                                                                                                                                                                                    312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAA 161
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 TyralaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa
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Ratio: 4.433
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1162 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
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                                                                                                                                                                                                                                                                                                                                                                         1262
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                                                  1412 T 1412
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                                                                                                  451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467
467 a 467
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                                                                                                                                                                                                               isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
                                                                                                                                                                                                                                                                  ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1361
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alignment_block:
US-09-488-265-25 x US-09-155-855-3
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Ratio: 4.396
Percent Similarity: 90.364
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GENERAL INFORMATION:
APPLICANT: KONDO, Hidemasa
APPLICANT: ANAZAWA, Hideharu
APPLICANT: KANEKO, Syunichi
APPLICANT: KANEKO, Syunichi
APPLICANT: NAGASHIMA, Tadashi
APPLICANT: TANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 81356/124
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CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER APPLICATION NUMBER: JP 084314
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ. ID NOS: 7
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                 462 GCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTAT 511
                                                                 412 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 461
                                                                                                                                                                                                        362 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 411
                                                                                                                                                                                                                                                        101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 211
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Percent Identity: 73.448
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| 417<br>1312<br>434<br>4362<br>1362   | - 6 0 H 8 6                             | 33 35 35   | 28<br>91<br>30<br>31   | 23<br>76<br>25<br>81<br>86   | 1:<br>5:<br>5:<br>5:<br>5:<br>6:<br>6:<br>6:<br>6:<br>71   |
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| 417 uGInGluProLeuValArgValLeuValAsnAspArgVaivaivaivaivaivaivaileuValAsnAspArgVaivaivaivaivaivaivaivaivaivaivaivaivaiva | .16<br>38<br>38<br>38<br>38<br>38<br>40 | 334 spaspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhebr 062 TTGAACGCCTACTTTGGGCTTCTCTCAGCAGCTACTATRPhebr 163 spaspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhebr 164 TTGAACGCTACTTGTGAGCTGACTTCTCTCAGAGACACATATGGTTT 164   1 | 284 eupheThrHisGlucluTrpIleA 912 AAGTACTACGGTTACGGTGCTGGT 912 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 334 hrhevalProSerIleArgGlnArgLeuGllAsnAspLeuSerGly\ 62 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTG 51 SerLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPh 51 SerLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPh 62 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCAATCTGTGA 64 TGTTCACGACGAATGGATTCAATACGACTACTTACAATCTTTGC 65 TGTTCACTCACGAATGGATTCAATACGACTACTTACAATCTTTGC 66 TGTTCACTCACGAATGGATTCAATACGACTACTTACAATCTTTGC | 151 ThrargasnilevalprophelleargSerSerGlySerSerargVal 212 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGC 111111111111111111111111111111111  |
| 1361<br>1361<br>450<br>1411<br>467   | 14141                                   | :A 1061<br>  0 350<br>'C 1111<br>  1 367<br>  1 384  | 30160  | 1 25<br>A 81<br>I 26<br>S 26<br>I 86<br>I 28<br>I 28   | .Il 167 .II 167 .II 561 .II 611 .II 611 .II 200 .II 20 |

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Result
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re greater than or equal to the score of the result being printed,
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| TION: TOON:  | 771.1<br>5669.6<br>669.6<br>554.5<br>544.5<br>544.3<br>333.7<br>333.7<br>14.0<br>14.0  |
| artin onsensu  | 466 4<br>466 4<br>475 2<br>475 4<br>487 4<br>487 4<br>483 3<br>443 3<br>439 3<br>443 3<br>443 3<br>443 3<br>443 3<br>443 3<br>447 3<br>447 3<br>479 1<br>479 1   |
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RESULT 2
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; Sequence 2, Application US/09121425
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Best Local Similarity
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EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
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CURRENT APPLICATION NUMBER: US/09/121,42
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                                                                                                          TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT
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                                   VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG
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Pred. No. 8.6e-221;
Pred. No. 8 19;
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NAME: Kass, Alan P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 104
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OTHER INFORMATION:
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LOCATION: 205
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Score 1902; DB 4;
Pred. No. 3.6e-192;
                  Length 465;
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Query Match

Best Local Similarity

77.0%; 77.1%;

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US-08-744-231-33
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                                           INFORMATION FOR SEQ ID NO:
                                                                        REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                          FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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US-07-923-724-8
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Sequence 8, Application US/07923724
Patent No. 5780292
GEMERAL INFORMATION:
APPLICANT: Nevalainen, Helena K
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Best Local Similarity
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NAME/KEY:
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                                                                                                                                   LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
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Helena K.M.
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Pred. No. 3.6e-192;
7; Mismatches 68;
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Best Local Similarity
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600
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APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UK 8 FILING DATE: 30-APR-1986 ATTORNEY/AGENT INFORMATION:
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241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
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GY: linear
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Turunen, Marja K.
Turunen, Marja K.
Fagerstr m, Richard B.
FERGURE Production of Phytase Degrading Enzymes
VENTION: in Trichoderma
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ork Avenue, Suite 600
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Pred. No. 2.3e-188;
4; Mismatches 75;
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                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Reed, Grant E.
                                                                                                                                                                                                                              FILING DATE: 29-APR-PRIOR APPLICATION DATA:
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                                                                                                                                       NAME: Reed, Grant E. REGISTRATION NUMBER: P-41,264
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07 FILING DATE: 19-MAR-1990
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07 FILING DATE: 31-JUL-1992
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                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/044,077
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amino acid
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                  467 amino acids
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Fagerstr m, Richard B.
Houston, Christine S.
ZENTION: Production of Phytase Degrading Enzymes
ZENTION: in Trichoderma
ZQUENCES: 69
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                                                                   (202)
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Paloheimo, Marja T.
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                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
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APPLICANT:
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                                                                                                                             COUNTRY:
                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                             USA
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US-08-151-574-32 ; Sequence 32, A

Patent No.

2, Application US/08151574 5436156

GENERAL INFORMATION:
APPLICANT: Robert

APPLICANT: APPLICANT:

Robert F.M. Van Gorcom Willem Van Hartingsveldt Petrus A. Van Paridon

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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DAFE: 31-JUL-1992
                                                                                            361
                                                                                                                   361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                            301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360
                                                                                                                                                                                    301 KYYGYGAGNPLGPAQGYGFYNELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLYADFS 360
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APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
                                                                                                                                                                                                                                          241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300
                                                                                                                                                                                                                                                                                241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                                                                           181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240
                                                                                                                                                                                                                                                                                                                                                                181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                                                                                                                                                                                                                                                                                                                                                        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180
                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SAISPDVPÄGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEATQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
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TOPOLOGY: not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 24-MAY
                                                                             HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REED,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.5%; Score 1866; DB 2; 74.5%; Pred. No. 2.3e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/374,652C
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; MOLECULE TYPE: protein US-08-151-574-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Cloning and Expression of Microbial TITLE OF INVENTION: Phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-MAY-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                  121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                            181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240
                                                                                                                                                                                                                                                                                                                                         121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300
                                                                                                                                                                                                241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG
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FILING DATE: 24-MAY-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MCVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Rudolf G.M. Luttin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.4%; Score 1862; DB 1; 74.5%; Pred. No. 6.1e-188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: ///
CITY: Palo Alto
CTATE: California
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TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SIJMONS,
APPLICANT: VERWOERD
TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08
FILING DATE: 02-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: \-\ 706141
                                                                                                                         ADDRESSEE: MUNICIPAL ROAD COMPRET: 755 Page Mill Road
           241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLGSLG 300
                                                                                 181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                                                                                                                                                                                                                                                                                              y match 75.4%; Score 1862; DB 1; Length 467; Local Similarity 74.5%; Pred. No. 6.1e-188; les 348; Conservative 44. Winner 1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: KENNEDY, BILL REGISTRATION NUMBER: 33,407
                                                                                                                                                                                                   61 SYISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEETQQNATTFDGKYAFLKTYN 120
                                                                                                                                                                                                                        61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
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                                                    KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240
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5593963
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOEKEMA, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEN, JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAN OOIJEN, ALBERT J. J.
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Conservative 44; Mismatches

75; Indels

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US-08-693-709-2
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US-08-693-709-2
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    Query Match
Best Local :
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                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                          MOLECULE TYPE: FRAGMENT TYPE: FEATURE:
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                      FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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 Local Similarity
                                                                 NAME/KEY: Signal LOCATION: 1...23
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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                                                                                                                                                                                                                                                                              NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/1 FILING DATE: 02-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 755 PAGE CITY: Palo Alto
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                        CENGTH:
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                                                                                                                                                                        amino acid
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5770413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA
                                                                                                                                                                                     467 amino acids
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SIJMONS, PETER C.
                                                                                          Signal Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                       protein internal
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Score 1862; DB 1;
Pred. No. 6.1e-188;
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US-08-419-448-32
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INFORMATION FOR SEQ ID NO:
                                                                                   APPLICATION NUMBER: US/08/
FILING DATE: 10-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H.
REGISTRATION NUMBER: 29,95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                  REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
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                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467
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                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Petrus A. Van Paridon
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: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning and Expression of Microbial
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 3, Application US/08819825
Patent No. 5866118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 467 amino acid
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APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
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Local Similarity 74.5%; Pred. No. 6.1e-188;
Local Similarity 44; Mismatches 75;
                                                                                                   COMPUTER: IBM CON
OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                STREET:
                                       APPLICATION NUMBER: US/08/819,825 FILING DATE: 18-MAR-1997
                                                                                                                                                                                                            ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
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                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                          10174-6401
                                                                                                                                                                                                                                                                                                405 Lexington Avenue,
                                                                                                                                            IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                    US-09-163-642-3
                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09163642 Patent No. 6221644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 348; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                          APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                       STREET: 405 Lexit
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 LYRYLYNDRYYPLHGCGYDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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REFERENCE/DOCKET NUMBER:
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COMPUTER:
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                                                                                                                                            405 Lexington Avenue, Suite 6400
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IBM Compatible
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US-09-233-510-32
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                                                                                                                                         Sequence 32, Application US/09233510
                                                                                                                             Patent No. 6350602
                                                                                          GENERAL INFORMATION: APPLICANT: Robert
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Best Local Similarity
                                   APPLICANT:
APPLICANT:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 APPLICANT:
                     APPLICANT:
                                                                                                                                                                                                                                 421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467
                                                                                                                                                                                                                                                      421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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REFERENCE/DOCKET NUMBER: 4758.200-US
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REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                            KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS
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           Robert F.M. Van Gorcom
Willem Van Hartingsveldt
Petrus A. Van Paridon
Annemarie E. Veenstra
Rudolf G.M. Luttin
Gerardus Selten
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FastSEQ for Windows Version 2.0
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
           421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                            361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP
                                                                361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                          301
                                                                                                                                  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATEPLNATLYADES
                                                                                                                                                                                241 QRLENDLSGYTLTDTEVTYLMDMCSFDTISTSTYDTKLSPFCDLFTHDEWINYDYLQSLK 300
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LENGTH: 467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    121
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                              61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEATQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 75.4%; Score 1862; DB 4; Local Similarity 74.5%; Pred. No. 6.1e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Murashige, Kate
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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348;
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1996-04-04
EARLIER FILING DATE: 1996-04-05
NUMBER: OF SEQ ID NOS: 7
SOTTWARE: PATENTIN VET. 2.0
SEQ ID NO 3
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Sequence 3, Application US/09155855

Patent No. 6139902

GENERAL INFORMATION:
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US-09-155-855-3
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Search completed: July Job time: 151 sec
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APPLICANT: ANAZAWA, Hideharu
APPLICANT: KANEKO, Syunichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NAGASHIMA, Tadashi
APPLICANT: TANCE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 81356/124
                                                                                                                                                                                                                                                                                                                                                                                                                             181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/B_COMB.pep:*
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     US-09-121-425-1
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US-08-686-435-33
US-08-744-231-3
US-08-744-231-1
US-08-744-231-1
US-08-744-231-1
US-08-744-231-1
US-08-744-231-1
US-08-151-574-32
US-08-146-424-20
US-08-146-424-20
US-08-149-448-32
US-08-149-448-33
US-09-155-855-1
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US-09-155-855-3
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| HILWGOY HALWGOY HATAFKG   | 9121<br>us I<br>USta<br>USTA<br>7-23<br>EPC<br>7-24<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10  | 44424443333331112  |
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| DES<br>   | 9<br>25<br>8.3<br>8.3  | -744-23<br>-744-23<br>-744-23<br>-744-23<br>-1619-62<br>-1639-68<br>-168-43<br>-974-23<br>-993-35<br>-993-35<br>-627-53<br>-993-35<br>-627-53<br>-993-35<br>-627-53<br>-993-35<br>-627-53  |
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| 58<br>50<br>1117<br>1117<br>120<br>120<br>120<br>120<br>120<br>133<br>133<br>140<br>90<br>90<br>90<br>90  | טי<br>מ  | 35, Appli<br>2, Appli<br>2, Appli<br>2, Appli<br>4, Appli<br>4, Appli<br>30, Appli<br>24, Appli<br>24, Appli<br>26, Appli<br>27, Appli<br>28, Appli<br>29, Appli<br>20, Appli<br>21, Appli<br>22, Appli<br>23, Appli<br>24, Appli<br>25, Appli<br>26, Appli<br>27, Appli |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/121,42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1997-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:consensus OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 KLGRCKRDDFVEGLSFARSGGNWAECFA 441
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                  391 LVRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                 332 IFFALGLYNGTKPLSTTSVESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGEGEKEP 390
                                                                                                                                                         308 GNPLGPAQGVGFANELIARLTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMIS
                                                                                                                                                                              273 GNPLGPAQGYGF-NELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVS
                                                                                                                                                                                                                                                                               215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                                                                                                                                                                                                                                 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDLIEAIQKNAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 86
                                                                                                                                                                                                                                         PGYTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGA 307
                                                                                                                                                                                                                                                            PGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGA 272
                                                                                                                                                                                                                                                                                                                       AFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTSSKSKAYSA-----TYNYTLGADDLTPFGENQMVNSGIKFYRRY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTSSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
                                                                           IFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQA---
LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.9%; Score 1902; DB 4;
81.8%; Pred. No. 3.8e-195;
ative 10; Mismatches 19;
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GENERAL INFORMATION:
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                                                                   Best Local Similarity
                                                                                     Query Match
                                                     Matches 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (201) 235-23
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Van Loon, APPLICANT: Mitchell, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acid
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NAME: Kass, Alan P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                                                                                LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 104
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                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 374
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2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
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amino acid
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SYSTEM: PC-DOS/MS-DOS
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                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                       75.9%; Score 1762.5; DB 4 77.4%; Pred. No. 3.4e-180;
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                                                                                                                                                                                                                                                                                              /note="potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="potential N-glycosylation site"
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                                                           Mismatches
                                                                                             DB 4;
                                                            48;
                                                           Indels 17; Gaps
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US-08-744-231-33
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                                                                                            TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                     REFERENCE/DOCKET NUMBER: CATELECOMMUNICATION INFORMATION: TELEPHONE: (201) 235-4205
MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBE: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MITCHEII, DAVIG
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Van Loon, Adolphus APPLICANT: Mitchell, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 AKELDGYSASWVVPFGARAYFETMQCKS-----EKEPLVRALINDRVVPLHGCDVDKL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 I-ETDGYAASWTVPFAARAYVEMMOCEAGGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                             REGISTRATION NUMBER: 32142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVTIPEGSGYNN 176
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/744,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                           Kass, Alan P
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                                                                           465 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                              Case Docket 9339
                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
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RESULT 5
US-08-688-435-12
US-08-868-435-12
; Sequence 12, Application US/08868435
; Patent No. 6291221
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                       353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
                                                                                                                                                                                                                                                                                               327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 374
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Pred. No. 3.4e-180;
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APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS

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; MOLECULE TYPE: protein US-08-868-435-12
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
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ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
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STREET: 340 K
CITY: Nutley
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         327
                                                                                                                                                                       291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSV 350
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440 KLGRCKRDAFVAGLSFAQAGGNWADCF 466
                                  410 KLGRCKLDDFVEGLSFARSGGNWAECF 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/868,435
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                                                                                                                                                                                                                                                                                                                                                                                                                                      27 NQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPDVPAGCRVTFAQVLSRHGARY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 72.7%; Score 1688; DB 4; Length 466; Local Similarity 74.3%; Pred. No. 3.3e-172;
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                                                                  ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                            NNTLDHGLCTAFEDSTLGDDAEANETAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                       ETVSLTDDAHTLSPFCDLFTATEWTQYNYLLSLDKYYGYGGGNPLGPVQGVGWANELMAR 326
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amino acidDGY: linear
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340 Kingsland Street
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US-08-744-231-12

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APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
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TELEFAX: (201) 235-236
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 18-APR-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
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                                                                                                                                                                                                                                                         175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/744,231
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                                                                                                                                                                                                                                                                                                                                                                                                                                             27 NOSTCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPDVPAGCRVTFAQVLSRHGARY 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                                                                                                                                                                                                         PTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146
ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                        LTRAPVHDHTCVNNTLDASPATFPLNATLYADFSHDSNLVSIFWALGLYNGTAPLSQTSV
                                                                                               LTHSPVQDHTSTNHTLDSNPATEPLNATLYADESHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                ETVSLTDDAHTLSPFCDLFTATEWTQYNYLLSLDKYYGYGGGNPLGPVQGVGWANELMAR 326
                                                                                                                                                                     DTVARTSDATOLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                          332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity 74.3 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
7: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoffmann-La Roche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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235-2363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.7%; Score 1688; DB 4; Length 466; 74.3%; Pred. No. 3.3e-172; ative 39; Mismatches 58; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08/424,757
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US-07-923-724-8
                                                                                                        Matches
                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Appr
                                                                                                                                                                                                                                        TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 861
FILING DATE: 30-APR-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 10;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,07/923,724
FILING DATE: 31-JUL-1000
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-APR-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
59 PTSSKSKKYSALIERIQKN-ATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                          27
                                                                                                                  Local Similarity
                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                             APPLICATION NUMBER: US 0/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 KLGRCKRDAFVAGLSFAQAGGNWADCF 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fagerstr m, Richard B.

VENTION: Production of Phytase Degrading Enzymes

VENTION: in Trichoderma
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Torkkeli, Tuula K.
Cantrell, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Paloheimo, Marja T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                             protein
                                                                                                          72.7%; Score 1688; DB 1; Length 467; 73.9%; Pred. No. 3.3e-172;
                                                                                                                                                                                                                                                                                                                                                                                                              UK 8610600
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 07/044,077
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                                                                                                                                                                                                                                                                                                                                 1050.0240004
                                                                                                Mismatches
                                                                                              59;
                                                                                              Indels
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                                                                                         Gaps
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US-08-609-426A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                          APPLICATION NUMBER: US OF STATE OF STAT
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/609,426A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fagerstr m, Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of
TITLE OF INVENTION: in Trichoderm
NUMBER OF SEQUENCES: 69
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       APPLICATION NUMBER:
                                                                                                                                                                               APPLICATION NUMBER: US 0
FILING DATE: 19-MAR-1990
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 LTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 DTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 DTVARTSDATQLSPECDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 YKALARNIVPEVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
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Turunen, Marja K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piddington, Christopher S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paloheimo, Marja T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nevalainen, Helena K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1996
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                                                                                                          US 07/044,077
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UK 8610600
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US-08-374-652C-2
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RELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                sequence 2, Application US/08374652C
Patent No. 5834286
                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
         APPLICANT: HOUSTON, CHRISTINES.

APPLICANT: CANTRELL, MICHAEL A.

TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                            APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                        440 ALGRCTRDSFVRGLSFARSGGDWAECSA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
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                                                                                                                                                                       MIETTINEN-OINONEN, ARJA S.
                                                                                                                                                                                         FAGERSTROM, RICHARD B.
                                                                                                                      PIDDINGTON, CHRISTOPHER S.
                                                                                                                                     RAMBOSEK, JOHN A.
                                                                                                                                                        TURUNEN, MARJA K.
                                                                                                                                                                                                                              NEVALAINEN, HELENA K.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.7%; Score 1688; DB 2; Length 467; 73.9%; Pred. No. 3.3e-172;
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                                                         PHYTATE DEGRADING
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; MOLECULE TYPE: protein
US-08-374-652C-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/I
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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    387
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                                                                                                            291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
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                                                                                                                                                                                                                                                                                                          147 YESLTRNIIPFIRSSGSSRVIASGEKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206
                                                                                                                                                                                                                                                                                                                                              118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/925,401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                    87 PTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146
                                                                                                                                                                                                                                                                                                                                                                                                          59 PTSSKSKKYSALIERIOKN-ATFKGKYAFLKTYNYTLGADDLTPFGENOMVNSGIKFYRR 117
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                                    ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                          LTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386
                                                                                                                                                     DTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326
                                                                                                                                                                         DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                               NNTLDPGTCTVFEDSELADTVEANFTATFAPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266
                                                                                                                                                                                                                                                                 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
ENITQTDGFSSAWTVPFASRLYVEMMQCQA-----EQEPLVRVLVNDRVVPLHGCPID 439
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410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 32:
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APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                 147
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207 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266
                      175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                     87
                                                                                                                                                          59 PTSSKSKKYSALIERIOKNA-TEKGKYAFLKTYNYTLGADDLTPEGENOMVNSGIKEYRR 117
                                                                                                                                                                                                          27 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California & Foerster 200 STATE: California
                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                              1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLGRHGARY 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                  YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206
                                                                                                     YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                      PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146
                                                                                                                                                                                                                                                                                       331;
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5436156
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Petrus A. Van Paridon
Annemarie E. Veenstra
Rudolf G.M. Luttin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robert F.M. Van Gorcom
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                                                                                                                                                                                                                                                                                72.6%; Score 1684; DB 1; 73.9%; Pred. NO. 8.9e-172; 73+1ve 40; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                   Length 467;
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Sequence 20, Apprin
Sequence 20, Apprin
Sequence 20, Apprin
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                                                                                                                                                                                                                                                                                              TELEFAX: (415) 494-079
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENOMVNSGIKFYRR 117
                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: KENNEDY, BILL
REGISTRATION NUMBER: 33,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 LTHSPVQDHTSTNHTLDSNPATEPLNATLYADESHDNTMYSIFFALGLYNGTKPLSTTSV 350
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                                                                                  1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                               331;
                                                                                                                                                                                                                                                               amino acids
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                                                                                                                             Conservative
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VENTION: THE EXPRESSION OF PHYTASE IN PLANTS
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HOEKEMA, ANDREAS
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                                                                                                                                        72.6%; Score 1684; DB 1; Length 467; 73.9%; Pred. No. 8.9e-172;
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                                                                                                                          40; Mismatches
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US-08-693-709-2
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Patent No. 5770413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                               FILING DATE: 02-NOV-1993
ATTORNEY AGENT INFORMATION:
NAME: MUTASHIGE, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
                                                                       INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                           FILING LANGE BUU CLASSIFICATION: 800 PRIOR APPLICATION DATA: 08/146,424 APPLICATION NUMBER: 02-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: THE EXPRESSION OF PHYTASE TITLE OF INVENTION: IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION UNMBER: US/08/693,709 FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VERWOERD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327
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                                   SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
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STATE: C
COUNTRY:
                                                                               TELEFAX: *- 706141
                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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STRANDEDNESS:
                                 ENGTH:
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                 amino acid
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                                                                                                             415-494-0792
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HOEKEMA, ANDREAS
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                                                                                                                                   415-813-5600
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,

Version #1.25

ZIP: 20006-1888

STATE: COUNTRY:

USA

APPLICANT:

Robert F.M. Van Gorcom
Willem Van Hartingsveldt
Petrus A. Van Paridon
Annemarie E. Veenstra
Rudolf G.M. Luttin

APPLICANT:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

Phytase 52

STREET:

ADDRESSEE:

E: Morrison & Foerster 2000 Pennsylvania Ave. N.W.,

Suite 5500

CITY: Washington

D.C

APPLICANT: APPLICANT:

Gerardus Selten

Cloning and Expression of Microbial

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Sequence 32, APP--
Sequence 32, APP--
Sequence 32, APP--
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GENERAL INFORMATION:
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MOLECULE TYPE: |
FRAGMENT TYPE:
FEATURE:
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                                                                                                                  440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467
                                                                                                                                                410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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                                Application US/08419448
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internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 467;
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US-08-819-825-3
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                                                                                                                                                                                                                                 Sequence 3, Application US/08819825 Patent No. 5866118
                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                       APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO:
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
STREET: 400
STREET: 400
TTMY: New York
                                                                                                                                                                                                                                                                                                                                                               410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 240
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08
FILING DATE: 10-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
                                                                                                                                                                                                                                                                                                                                             440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                              ENITQTDGFSSAWTVPFASRLYVEMMQCQA------EQEPLVRVLVNDRVVPLHGCPVD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
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    New York
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; Sequence 3, Application US/09163642
; Patent No. 6221644
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GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 331; Conservative 40; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                              440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467
                                                                                                                                                                                                                     410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 YKALARNIYPFYRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPYINVIIPEGSGY 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146
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N: 435
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TITLE OF INVENTION:

Polypeptides Having Phytase Activity

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US-09-163-642-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/08/819
APPLICATION UNMBER: 1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambliris, Elias J.
REGISTRATION UNMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                              267 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326
                                                                                                                                                                                                                 207
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/163,642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
               410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                 351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467
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                                                                                                                                                                                                                                                                                                                                                    YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86
                                                                                                                                                                                                                                                                    NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF
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                                                                 New York
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.6%; Score 1684; DB 4; Length 467; 73.9%; Pred. No. 8.9e-172; ative 40; Mismatches 59; Indels 18
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                                                                      -EQEPLVRVLVNDRVVPLHGCPVD 439
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Search completed: July 3, 2002, 09:33:13 Job time: 152 sec

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Database: Issued_Patents_AA:*
Database sequences: 231628
Database length: 24425594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      About: Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -O-/Cgn2_1/USPTO_Spool/US0448265/runat_03072002_091241_4286/app_query.fasta_1.4477
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 2282.00
Ratio: 5.234
Percent Similarity: 98.866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: U5/09/121,425
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
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TITLE OF INVENTION: Consensus Phytases
FILE REFERENCE: CONSENSUS Phytases 13239
117 eTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:consensus
                                           101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysph
                                                                                                              379 GACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGTATTAAGTT 428
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                                                                                                                                                                                                                                                                                                                    279 GGCTTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCA 328
                                                                                                                                                                                                                                                                                                                                                                                   229 CAAGITITGTCTAGACACGGTGCTAGATACCCCAACTTCTTCTGCGTCTAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 AATCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTT
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                                                                                                                                                                                84 ysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100
                                                                                                                                                                                                                                                                                                                                                                51 GlnVaiLeuSerArgHisGlyAlaArgTyrProThrSerSerLysSerLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 luSerAlaIleSerProAspValProAspAspCysArgValThrPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 uIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGl 17
                                                                                                                                                                                                                         AGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 378
                                                                                                                                                                                                                                                                         sAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAlaThrAlaPheL
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Percent Identity: 97.732
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1.9e-28
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                                                                                                                                                                                                                                                                                                                                                                                                                 1079 CTCACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAAC 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1029 CTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCT 1078
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                                                                                                                                                                     1229 AAATGATGCAATGTCAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
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               1329 ATGTAAGAGAGAGACTTCGTTGAAGGTTTTGTCTTTCGCTAGATCTGGTG 1378
                                                                                                             1279 AACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAGTTGGGTAG 1328
                                                                                                                                                                                                                                                                                                                                                                             317 pSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAs 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       979 TTGACTCACTCCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 GluLeuSerProPheCysAlaLeuPheThrHisAspGluTrpArgGlnTy 267
                                                                                                                                                                                                                                                                                                     384 luMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400
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gCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyG 434
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1379 GTAACTGGGCTGAATGTTTCGCT 1401

## seq\_name: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:US-09-121-425-2 ; OTHER INFORMATION: Descript: ; OTHER INFORMATION: sequence US-09-121-425-2 seq\_documentation\_block: alignment\_block: US-09-488-265-28 x US-09-121-425-2 alignment\_scores: Quality: 2270.00 Ratio: 5.136 Percent Similarity: 90.760 GENERAL INFORMATION: Sequence 2, Application US/09121425 Patent No. 6153418 Align seg 1/1 to: US-09-121-425-2 from: 1 to: 467 SEQ ID NO 2 EARLIER APPLICATION NUMBER: EPO 97112688.3 EARLIER FILING DATE: 1997-07-24 NUMBER OF SEQ ID NOS: 20 FILE REFERENCE: consensus phytases CURRENT APPLICATION NUMBER: US/09/1 CURRENT FILING DATE: 1998-07-23 APPLICANT: Lehmann, Martin TITLE OF INVENTION: Consensus Phytases SOFTWARE: PatentIn Ver. 2.0 ORGANISM: Artificial Sequence TYPE: PRT FEATURE: LENGTH: 467 101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150 201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTTGTCTAGACACGGTG 250 151 TACTOTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200 351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400 301 17 rSerGlyThrAlaLeuGlyProArgGlyAsnSerHisSerCysAspThrV 34 51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100 67 51 TyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAspVa 84 laArgTyrProThrSerSerLysSerLysAlaTyrSerAla...... 97 1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50 97 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350 lProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyA 84 .ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluA 114 Description of Artificial Sequence:consensus US/09/121,425 Percent Identity: 89.733 67

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1191 TICTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAAT 1240
                                                                                                                                                                  1091 CTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
                                                                                                                                                                                                                                                                                                                                                                  1041 TACTITICCATTGAACGCTACTITGTACGCTGACTTCTCTCACGACAACA 1090
                                                                                                                                                                                                                                                      364 erMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
                                                                                                                                                                                                                                                                                                                                           347 aThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnS 364
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                                                                                   aSerTrpThrValProPheGlyAlaArgAlaTyrValGluMetMetGlnC 414
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; MOLECULE TYPE: US-07-923-724-8
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GENERAL INFORMATION:
APPLICANT: Nevala
                                                                                                                                                                                              TELEFAX: (202) 371-25.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: UK 8
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
DETOR ABBLICATION TO THE PRIOR APPLICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1391 AATGTTTCGCT 1401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
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                                                                    TOPOLOGY:
                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/044,077 FILING DATE: 29-APR-1987
                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Cimbala, Michele A. REGISTRATION NUMBER: 33,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/923,724
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                                                                                                   amino acid
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                                                                                                                             467 amino acids
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                                                                        linear
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Paloheimo, Marja T.
                                                                                                                                                                                                                                                                                  (202)
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                              protein
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alignment\_scores:

Quality: 1879.00

Length:

467

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alignment_block:
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                                        751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
                                                                                                                             701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
                                                                                                                                                                                                            651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
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89.507
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Percent Identity: 75.589
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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-609-426A-8
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                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08609426A Patent No. 5830733
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                          CORRESPONDENCE ADDRESS
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                     ADDRESSEE:
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                                                                                                                                                                                                                        Nevalainen, Helena K.M.
Paloheimo, Marja T.
Miettinen-Oinonen, Arja S.K.
Torkkell, Tuula K.
Cantrell, Michael
                                                                             Turunen, Marja K.

Pagerstr m, Richard B.

Houston, Christine S.

VENTION: Production of Phytase Degrading Enzymes

VENTION: in Trichoderma
                                                                                                                                                                                 Piddington, Christopher S. Rambosek, John A.
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alignment_block:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
            151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
                                                                                                                                                                                 201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGCGTG 250
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
1.00,07/496,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                               67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA
                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                    17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrv 34
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APPLICATION NUMBER: UK 86
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
                                                                                                                                                                                                                                                                                     51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                       1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValTh 17
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/609,426A FILING DATE: 01-MAR-1996
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       Quality: 1879.00
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SYSTEM: PC-DOS/MS-DOS
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Length:
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1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
                                            1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
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                                                                                                                                                                                                                                                                                                                        1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
                                                                                                 367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384
                                                                                                                                                                                               334 spAspThrSerSerAsnHisThrLeuAspSerAsnProAlaThrPhePro 350
                                                                                                                                                                                                                                                                                                                                                                                               317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334
                                                                                                                                                                                                                                                                                                                                                                                                                          951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-652C-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: NEVALA
APPLICANT: PALOHE
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                      INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/374,652C FILING DATE: 24-MAY-1995 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/925,401
APPLICATION NUMBER: US 07/925,401
SEQUENCE CHARACTERISTICS:
                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                      FILING DATE: 31-JUL-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                            TELEFAX:
                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                              TELEPHONE:
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PALOHEIMO, MARJA T.
FAGERSTROM, RICHARD B.
MIETTINEN-OINONEN, ARJA S.
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                                            202-371-2540
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                                                              202-371-2600
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US-08-374-652C-2
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601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
                                                                                                                                                    184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
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                                                                                                                                     Patent No. 5436156
                                                                                                                      GENERAL INFORMATION:
                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robert F.M. Van Gorcom
Willem Van Hartingsveldt
Petrus A. Van Paridon
Annemarie E. Veenstra
Rudolf G.M. Luttin
Gerardus Selten
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alignment_block:
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Quality: 1875.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, Kate H.
REGISTRATION NUMBER: 29,95
301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
                                                                     151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCCAGACGT 200
                                                                                                                                        201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
                                                                                                                                                                                                                                                                                101 TIGACGGTGGTTACCAATGTTTCCCCAGAAATTTCTCACTTGTGGGGTACC
                                                                                                      67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84
                                                                                                                                                                           51 TyralaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa
                                 84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
                                                                                                                                                                                                                                               34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50
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                                                                                                                                                                                                                                                                                                                  17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrv 34
                                                                                                                                                                                                                                                                                                                                                    51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                     1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/151,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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545 Middlefield Road, Suite 200
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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451 GCTAGAAAGATIGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
                                                                                                                                                                                                            1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
                                                                                                                                                                                                                                                                          1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
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                                                                                                                                            1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
                                                                                                                                                                                                                                                                                                                                                                        801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
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                                                                                                                                                                                                                                           334 spaspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350
                                                                                                                                                                                                                                                                                                                                        951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
                                                                                                                                                                           351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367
                                              SerGluAlaSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-146-424-20
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                                                                                                                                                          ; TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-146-424-20
alignment_block:
US-09-488-265-28 x US-08-146-424-20
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Patent No. 5
                                                                                                           alignment_scores:
                                               Quality: 1875.00
Ratio: 4.475
Percent Similarity: 89.722
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                                                                                                                                                                                                                                                                       TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
NUMBER OF SEQUENCES: 31
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                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: KENNEDY, BILL
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: /55 Page CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 02-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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5593963
                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                          (415) 813-56
(415) 494-0792
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                                                                                                                                                                                                      linear
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02-NOV-1993
                                                                                                                                                                                 protein
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                                                         Percent Identity:
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                                                                                               Length:
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Align seg 1/1 to: US-08-146-424-20 from: 1 to: 467
851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
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                                                                                                                                                                                                                                                                                                     234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
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                                                                                                                                                  CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
                                                                                                pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284
                                                                                                                                                                                                  ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267
                                                                                                                                                                                                                                                                                                                                                     TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
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| ProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84
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seq_documentation_block:
; Sequence 2, Applicatio
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: VAN OOIJEN,
APPLICANT: RIETVELD, K
APPLICANT: HOEKEMA, AN
APPLICANT: PEN, JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1401 T 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
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CURRENT APPLICATION DATA:
                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: THE EXPRESSION OF PHYTASE TITLE OF INVENTION: IN PLANTS
                                                                                                                                                                                                                                                                                                                              APPLICANT: SIJMONS, PETER C. APPLICANT: VERWOERD, TEUNIS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1151 CITCIGITGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
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                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 a 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
                                                                                                                                                                                   STREET: 755 PAGE CITY: Palo Alto
                      SOFTWARE:
                                          OPERATING SYSTEM:
                                                                                 MEDIUM TYPE:
                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
                                                                COMPUTER:
                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Application US/08693709
5770413
                                                                                                                                                                      CA
                                                                                                                                                                                                                                                                                                                                                PEN, JAN
SIJMONS, PETER C.
               FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                 HOEKEMA, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                      VAN OOIJEN, ALBERT J.J
                                                           IBM Compatible
                                                                                    Diskette
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NAME/KEY: Signal Sequence; LOCATION: 1...23; OTHER INFORMATION: US-08-693-709-2
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US-09-488-265-28 x US-08-693-709-2
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Ratio: 4.475
Percent Similarity: 89.722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-693-709-2 from: 1 to: 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 415-813-5600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                        201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
                                                                                                                                                                                                                                                                                                                                                                                 151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
                                                                                                                      101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117
                                                                                                                                                                                                                                 401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
                                               117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134
                                                                                                                                                           301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
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                                                                                                                                                                                                                                                                                                                                                                                                                    34 alaspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
                                                                                                                                                                                                 REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
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: 467 amino acids amino acid
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internal
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151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167
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                  1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
                                                                                                                                                                                                                                                                                                       1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
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                                                                                                                                                                                                                                                           367 rileLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                         351 LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367
434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
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                                                                                                                               AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
                                                                                                                                                                        ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417
                                                                                   uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
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alignment_block:
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Ratio: 4.475
Percent Similarity: 89.722
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                                                                                                                                                                                                        US-09-488-265-28 x US-08-419-448-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 32:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Murashige, Kate H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1401 T 1401
                                     51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                   1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 10-APR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murashige, Kate H. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2000 Penr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV
                                                                             MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robert F.M. Van Gorcom
                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morrison & Foerster
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901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
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                                                                                                                                                                                                 284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
                                                                                                                                                                                                                                                                                                267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284
                                                                                                                                                                                                                                                                                                                                               801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
                                                                                                                                                                                                                                                                                                                                                                                                 234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167
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Patent No. 5866118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1101 TATTTTCTTCGCTTTGGGTTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
                       TELEFAX: 212 867 0298 INFORMATION FOR SEQ ID NO:
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APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467 a 467
                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/819,825
                                                                 REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 47!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 405 Les
CITY: New York
STATE: New York
                                                                                                                                                 NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                       FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
7: U.S.A.
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                                                    212 867 0298
                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
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US-08-819-825-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-819-825-3 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-488-265-28 x US-08-819-825-3
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                                                                                                                                                                                                                                                                                                                         151 ThrargasnIleValProPheIleArgSerSerGlySerSerArgValIl
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217 lPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234
                                                                                                    601 CCAGAAGGATCCGGTTACAACAACACTTTTGGACCACGGTACTTGTACTGC 650
                                                                                                                                                                                                    551 ACCCAGGITCTCAACCACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa
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                                      TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
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Ratio:
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     GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                        Patent No. 6221644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1351 GAAGGTTTGTCTTTTCGCTAGATCTGGTGGTAAACTGGGCTGAATGTTTCGC 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  851 TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
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                                                                                                                                                                                                                                 Application US/09163642
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-163-642-3 from: 1 to: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-488-265-28 x US-09-163-642-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                    351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
                                                                                                                                                           151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
                                                                                                                                                                                                                        201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTTGTCTAGACACGGTG 250
                                                                                                                                                                                                                                                                                                                                                                                                       101 TIGACGGIGGTIACCAAIGTITCCCAGAAATTICTCACTIGIGGGGIACC 150
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APPLICATION NUMBER: US/08
FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
                                                                                                                       84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
                                                                                                                                                                                                   67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA
                                                                                                                                                                                                                                                                                    51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa
                                                                                                                                                                                                                                                                                                                                                                34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50
                                                                                                                                                                                                                                                                                                                                                                                                                                             17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/163,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17
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SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 10174-6401
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CITY: New York
STATE: New Yorl
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: 4.475
: 89.722
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                  1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
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                                                                                                                                                        384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-233-510-32
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            alignment_block:
                                                                                                     alignment_scores:
                                                                                                                                                         US-09-233-510-32
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US-09-488-265-28 x US-09-233-510-32
                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
                                                                                                                                                                                                                         TELEFAX: 415-327-2951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acid
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/6. FILING DATE: 24-MAY-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: 115-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Menlo Park
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                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                      NAME: Murashige, Kate
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,
                                                   Quality: 1875.00
Ratio: 4.475
milarity: 89.722
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                                                                                                                                                                                                                                467 amino acids
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                                                                                                                                                                                                                                                                                  415-327-2951
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                                                                                                                                                                                                                                                                                                                                                                                                                              07/688,578
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                                                       Percent Identity:
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                                                                                          Length:
                                                       0
75.589
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Align seg 1/1 to: US-09-233-510-32 from: 1 to: 467
801 CACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTT 850
                                                                                                                                                                    251
                                                                                                                                                                              751 ACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGA 800
                                                                                                                                                                                                                               234 hrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal
                                                                                                                                                                                                                                                        701 TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
                                                                                                                                                                                                                                                                                                               217 1PheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234
                                                                                                                                                                                                                                                                                                                                 651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
                                                                                                                                                                                                                                                                                                                                                                                         201 SerGluAlaSerSerAsnAsnThrLeuAspProGlyThrCysThrVa
                                                                                                                                                                                                                                                                                                                                                                                                               601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 ACCCAGGTTCTCAACCACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGATTAT 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGGTAAGTACGCTTTCTTGAA 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34
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                                                                           pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284
                                                                                                                                                       ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG}
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| Seq.documentation_block: Sequence 33, Application US/08868435 Patent No. 6291221 GENERAL INFORMATION: APPLICANT: Van Loon, Adolphus APPLICANT: Witchell, David TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS: ADDRESSEE: Hoffmann-La Roche Inc. STREET: 340 Kingsland Street CITY: Nutley STATE: New Jersey COUNTRY: United States of America ZIP: 07110 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/868,435 FILING DATE: CLASSIFICATION NUMBER: 08/744,231 APPLICATION NUMBER: 08/744,231 | seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-868-435-33 | 1401 T 1401<br>1<br>467 a 467 | 1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGC 1 ::: | 1301 ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1<br> | 1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1<br> ::: | 1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGA 1<br> | 1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1<br>  :::      :::    ::: | 1101 TATTITCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA     ::: | 1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC       ::: | 1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA<br> | 951 TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG<br>    ::: | 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT<br>          :::                    ::: |
|--|--|-------------------------------|---|---|---|---|--|---|---|---|---|--|
|  |  |                               | 400<br>67   | 350<br>50   | 300<br>34   | 250<br>17   | 200  | 1150<br>384   | 1100<br>367   | 1050<br>350   | 1000  | 950<br>317   |

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alignment_scores:
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INFORMATION FOR SEO ID NO: 33
SEQUENCE CHARACTERISTICS:
LENCTH: 465 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 1867.00
Ratio: 4.477
Percent Similarity: 89.293
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REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEPAX: (201) 235-2363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                        201 TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTCTCTAGACACGGTG 250
                                                                                                                                                                                        151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
                                                                                                                                                                                                                                                                                    101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
                                                                                                                                                                                                                                     33 alAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeuTrpGlyGln 49
                                                                                                                                                                                                                                                                                                                             17 gValSerAlaAlaProSerSerAlaGly...SerLysSerCysAspThrV 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC
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OTHER INFORMATION: /note="potential N-glycosylation site"
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OTHER INFORMATION: /note="potential N-glycosylation site"
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                                                                                                                                          TyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLe 66
                                            Kass,
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1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
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                                                                                                                                                                                                                                                                                                                   1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
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382 hrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal
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                                                                                                                                                                                                                                                                                                                                                                  eGlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
                                                                                       rIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgT 382
                                                                                                                                                                                   LeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSe
                                                                                                                                                                                                                                                                             spHisThrSerThrAsnSerThrLeuValSerAsnProAlaThrPhePro 348
                                                                                                               TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
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         398
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ. ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TYPE: amino acid
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                            FEATURE:
                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 isGlyCysAspValAspLysLeuGlyArgCysLysLeuAsnAspPheVal 448
                               LOCATION: 119
OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                  NAME/KEY: misc_feature LOCATION: 119
NAME/KEY: misc_feature
                                                                                                                        OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                   LOCATION:
                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/744,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGl 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                 linear
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alignment_scores:
Quality: 1867.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-488-265-28 x US-08-744-231-33
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                    551 ACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
                                                              166 eAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaA 183
                                                                                     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
                                                                                                                                                    150 AlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIl
                                                                                                                                                                                                                                     133 lnGlnLeuValAsnSerGlyTleLysPheTyrGlnArgTyrLysAlaLeu 149
                                                                                                                                                                                                                                                               401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
                                                                                                                                                                                                                                                                                                                                116 sThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluG 133
                                                                                                                                                                                                                                                                                                                                                       351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
                                                                                                                                                                                                451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
                                                                                                                                                                                                                                                                                                                                                                                                                    301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 laArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyAr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note="potential N-glycosylation site"
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OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 374
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         to: US-08-744-231-33 from: 1 to: 465
/note="potential N-glycosylation site"
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Percent Identity: 76.017
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                                                                                                                                                      166
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1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1101 TATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTA 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1051 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATC 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
                                                                                315
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                                                                                                                                                                                                                                                                                                                                                                                                                                      332 spHisThrSerThrAsnSerThrLeuValSerAsnProAlaThrPhePro 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                651 TTTCGAAGACTCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTT 700
465 r 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spProGlyAla...ThrAsnArgAlaAlaProAlaIleSerValIleIle 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eGlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAs 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euPheAlaProAspIleArgAlaArgAlaGluLysHisLeuProGlyVal 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTT 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLy 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGTTTCGCTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
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                                                                                                                                                                                                                   ACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
                                                                                                                                                                                                                                                          uLysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuH 432
                                                                                                                                                                                                                                                                                                                                                    rIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgT 382
                                                                                                                                                                       isGlyCysAspValAspLysLeuGlyArgCysLysLeuAsnAspPheVal 448
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seq\_name: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:US-09-155-855-3

seq\_documentation\_block:

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; ORGANISM: Aspergillus niger US-09-155-855-3
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APPLICANT: KONDO, Hidemasa
APPLICANT: ANAZAWA, Hideharu
APPLICANT: KANEKO, Syunichi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 467
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE FILE REFERENCE: 81356/124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TANGE, Tatsuya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACC 150
                                                           134 lnGluLeuValAsnSerGlyValLysPheTyrGlnArgTyrGluSerLeu 150
                                                                                                                                                                                                                                                                                  301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
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                                                                                                          401 ACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
                                                                                                                                                                                                 351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAA 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrAlaProPhePheSerLeuAlaAsnLysSerAlaIleSerProAspVa
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                GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACACGGTG 250
                                                                                                                                                                                                                                                                                                                              laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
                                                                                                                                                                                                                                                                                                                                                                                                                        lProAlaGlyCysHisValThrPheAlaGlnValLeuSerArgHisGlyA
                                                                                                                                                     sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134
Quality: 1860.00
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90.150
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                                                                                                                                                                               Percent Identity:
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| CTGCTGAAAGTTCATTGAAGGTTTCCATAGTTGCTG   ::::::::::::::::::::::::::::::::::::  | 1301 ACGGTT<br>      <br>434 isGlyC<br>1351 GAAGGT<br>::: | 401 ValPrc 251 AAAGGA 1:::   417 uGlnGl | TCI   | ω o ω c                            | 01 L<br>01 L<br>51 T<br>17 1                             | 51 TGTTC                                   | /51 ACTTT :::   251 SerLe 801 CACTG     : : 267 pThr1        | :    <br>217  | TTC                                     | 551 ACCCA<br>     <br>184 spPro         | 501 TGCTT<br>     <br>167 eAlas            | 151 ThrAr    |
|--|---|---|---|------------------------------------|--|--|--|---|---|---|--|--------------|
| CATTGAAGGTTTCCAATCTGCTAAGTTGCTA<br>elledlul  | TGTTTGACA   | heAlaSerAr<br>CCATTGGTTA                | CTTCGCTTTGGG :          uPheAlaLeuGl TTGAATCTATTG ::   :::   laGluAsnIleT | CTTCTACTAACC                       | TyrGlyHisGly  TyrGlyHisGly  CGCTAACGAATT  :              | CTCACGACGAA<br>     :::   <br> hrHisGluGlu | ACTGACGAAGA         ThraspThrGl CGCTAGAACTT :::: eSerThrSerT | .uAspSerGluL<br>.uAspSerGluL<br>.CTCCAGCTATT<br>::   :::                            | GGATCCGGTTA<br>:::   <br>AlaserThrse    | TTCTCAACCA<br>:::      <br>gAlaGlnPrc   | TGCTGAAAAGT<br> ::::::    <br> rGlyAsnLysP | gAsnIleValPr |
| CCAATCTGCTAAGTTGCTATTACTTACTTACTTACTTACT   | GTTGGGTAGAT   | etTyrValcetTyrValc                      | TTGTACAAC   | ACACTTTGGACT                       | AlaGlyAsnPr<br>GATTGCTAGAT                               | GGATCCAATAC                                | TGTTTACT:  :::      ThrTyrLe ACGCTACTC     alAspThrI         | ::::       uAlaAspAsp uAlaAspAsp GAGCTAGATT             rgGlnArgLe                  | AACAACACTTT                             | ACCAAGCTTCT<br>   :::   <br> yGlnSerSer | CATTGAAGGTT<br>          <br> CattgaaggtT  | oPheIleArgSe |
| TTTGGCTG LICHLYSA LICELLYSA LICELLYSA LICELLYSA LICELLYSA LICELTGGTGTGGATCATT LICELTACTGG LILILI THARALAT THARALAT THARALAT THARALAT TOTGCTT LILILI TGLYVAL TGGACTGGT TITCCCA TGGACTGGT TTTGGACTG TTTTGGACTG TTTTTGGACTG TTTTGGACTG TTTGGACTG TTTTGGACTG TTTTGGACTG TTTTGGACTG TTTTGGACTG TTTTGGACTG TTTGGACTG TTTTGGACTG TTTTTT | TAAGAGAGACG         :   SThrArgAspS ACTGGGCTGAA           | I GAT GCAATGT                           | ACCAAGCCATI   | CTAACCCAGCT                        | LeuGlyProTh GACTCACTCTC                                  | CTACTTGC                                   | TGGACATGTG   | :        <br>eGluAlaAsnP<br>eGluAlaAsnP<br>AAGCTGACTTG<br>        <br>         <br> | GACCACGGT/<br>   <br>   <br> AspProGly1 | CAGTTATTAAC<br>      :::<br>roLysIleAsp | CCAATCTGCTA                                | rSerGlySerSe |
|  | ACTTCGTT 1 ::      cerpheval 4 TGTTTCGC 1                 | CAAGCTGA 1                              | GTCTACTA     :::  suSerSerT CTTGGACT ::      CLTTGGACT ::                 | TTTCCCA         rPhePro TGATATC :: | CAAGGTGT           GInGlyVa  AGTTCAAG      :::  OValHiSA | CTTGGGT<br>    :::                         | TCCATTCGA         sSerPheAs TCTGTGCTT                        | <br>heThrAlaT<br>CCAGGTGTT<br>     <br>SerGlyVal                                    | TGTACTGC<br>     ::<br>CysThrva         | GTGATCAT                                | AGTTGGCT                                   | erArgValIl   |

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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-08-609-426A-8
US-08-69-46-424-20
US-08-693-709-2
US-08-19-425-3
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| 1  | Query Match<br>Best Local Sim<br>Matches 431;                 | SSULT 1  1.09-121-425-1  5:09-121-425-1  Sequence 1, Application US/09  Patent No. 6153418  GENERAL INFORMATION:  APPLICANT: Lehmann, Martin  TITLE OF INVENTION: Consensus  FILE REFERENCE: consensus ph;  CURRENT FILING DATE: 1998-07  EARLIER APPLICATION NUMBER: 1  CURRENT FILING DATE: 1997-07.  NUMBER OF SEQ ID NOS: 20  SOFTWARE: Patentin Ver. 2.0  SOFTWARE: PAT  TYPE: PRT  ORGANISM: Artificial Sequence  PEATURE:  OTHER INFORMATION: sequence  OTHER INFORMATION: sequence | 28 1761<br>29 1719<br>30 1719<br>31 1334<br>32 1313.5<br>34 1313.5<br>35 802.5<br>36 798.5<br>37 798.5<br>39 795.5<br>40 778.1<br>41 778<br>42 347.5  |
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|  | Score 2282; DB 4; I<br>Pred. No. 1.2e-230;<br>; Mismatches 7; | ALIGNMENTS  21425  Phytases tases 13239 \$\$709/121,425 23 90 97112688.3 24  on of Artificial Sequence:c   | US-08-744-231-2 US-08-868-435-31 US-08-744-221-31 US-08-163-642-2 US-09-163-642-2 US-08-98-359-24 US-08-993-359-24 US-08-993-359-25 US-08-993-359-25 US-08-993-359-25 US-08-993-359-26 US-08-993-359-26 US-07-627-539G-2 US-07-627-539G-2 US-07-627-724-2 US-08-609-426A-2  |
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                                               VPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460
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                               VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG
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Pred. No. 2.4e-229;
3; Mismatches 7;
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APPLICATION NUMBER: US 07/
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 861
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Climbala, Michele A.
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                                                                                                                                        Matches
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/923,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                       Local
                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120
                                61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                      1 MGVFVVLLSTATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLMGTYSPYFSLADE 60
                                                                  MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
                                                                                                                                          353;
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                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                               467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fagerstr m, Richard B. //PATION: Production of Phytase Degrading Enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miettinen-Oinonen, Arja S.K.
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                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sterne, Kessler, Goldstein & Fox
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                                                                                                                                                                                                                                         protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in Trichoderma
                                                                                                                                                       76.3%; Score 1879; DB 1; 75.6%; Pred. No. 2.4e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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                                                                                                                                                                                                                                                                                                                                                                                                               33,851
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                                                                                                                                                                                                                                                                                                                                                                                                    1050.0240004
                                                                                                                                          Mismatches
                                                                                                                                                                          Length 467;
                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                 APPLICATION NUMBER: (FILING DATE: 29-APR-PRIOR APPLICATION DATA:
                                                                                           APPLICATION NUMBER: US 07/490,...
FILING DATE: 19-WAR-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/044,077
                                                                                                                                                                             APPLICATION NUMBER: US 0: FILING DATE: 31-JUL-1992 PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Piddington, Christopher APPLICANT: Rambosek, John A. APPLICANT: Turunen, Marja K. APPLICANT: Fagerstr m, Richard B. APPLICANT: Houston, Christine S. TITLE OF INVENTION: Production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 01-MAI CLASSIFICATION: 43:
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                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                     FILING DATE:
                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1100 New CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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Torkkeli, Tuula K.
Cantrell, Michael
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Paloheimo, Marja T.
                                                                                                                                                                                                                                                                               01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                       29-APR-1987
                                 30-APR-1986
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                                                                                                                                                                                                                     US 07/923,724
                                                   UK 8610600
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US-08-374-652C-2
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APPLICANT:
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                                                                                                                                                                APPLICANT:
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                    NUMBER OF SEQUENCES:
                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                        APPLICANT:
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REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
STREET:
CITY: V
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WASHINGTON
             1100 NEW YORK AVENUE,
                                                                                                                                        CANTRELL, MICHAEL A.
                                                                                                                                                                                                                                FAGERSTROM, RICHARD B.
MIETTINEN-OINONEN, ARJA S.
                                                                                                                                                                               PIDDINGTON, CHRISTOPHER S.
                                                                                                                                                                                                                   TURUNEN, MARJA K.
                                                                                                                                                                                                   RAMBOSEK, JOHN A.
                                                                                                                                                                                                                                                                         PALOHEIMO, MARJA
                                                                                                                                                                                                                                                                                       NEVALAINEN,
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                                                                              RECOMBINANT CELLS, DNA CONSTRUCTS,
VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
ENTYMES IN DESIRED RATIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.3%; Score 1879; DB 2; 75.6%; Pred. No. 2.4e-188; 75.6%; Mismatches 73;
                                                                      94
                                                                                                                                                                                                                                                                                         HELENA K.M.
               SUITE 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600 TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/925,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                           241 QRLENDLSGYTLTDTEVTYLMDMCSFDTISTSTYDTKLSPFCDLFTHDEWIHYDYLQSLK 300
                                                                                                                                                                                                                                                                                                                           181 KLADPGSOPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                 121 YTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFOSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 31 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/
FILING DATE: 27-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                 421 LYRVLYNDRVVPLHGCAYDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                 301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS
                                                                                                                                                                                                                                               241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                                                       181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGVFVVLLSIATLEGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
                                                                                                                                                                                                                                                                                                                                                                               SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120
                                                                                                           HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467
                                                                       HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP
                                                                                                                                                                                       KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATEPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-1995
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75.6%;
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Pred. No. 2.4e-188;
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US-08-151-574-32
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                          Matches 353;
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APPLICANT:
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TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 07/688,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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STATE: California
                                                                                                                                                                                 121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300
                     241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                      181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240
                                                                                           181 KLADDGSQPHOASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-327-7250
                                                                                                                                                                                                                      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120
                                                                                                                                                                                                                                         1 MGVSAVLLPLYLLSGYTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                   1 MGVFVVLLSIATLEGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLMGTYSPYFSLADE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petrus A. Van Paridon
Annemarie E. Veenstra
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                                                                                                                                                                                                                                                                                                                                                                              76.2%; Score 1875; DB 1; 75.6%; Pred. No. 6.3e-188; ative 41; Mismatches 73;
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Best Local (
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                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NÚMBER: 33,407
REFERENCE/DOCKET NUMBER: 441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: /JJ
CITY: Palo Alto
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                           TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 02-NO
                                                                                       1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
                                                                                                          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME:
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                             SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120
                                                        SAISPDVPDDCRVTFVQVLSRHGARVPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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                                                                                                                                                                                                                                                                                          467 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             755 Page Mill Road
                                                                                                                                                         Conservative
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HOEKEMA, ANDREAS
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                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                      76.2%;
75.6%;
                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                 44615-20011.24
                                                                                                                                                                 Score 1875; DB 1;
Pred. No. 6.3e-188;
                                                                                                                                                         Mismatches
                                                                                                                                                      73;
                                                                                                                                                                                 Length 467;
                                                                                                                                                   Indels
                                                                                                                                                     0;
                                                                                                                                                Gaps
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US-08-693-709-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5770413 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08693709 Patent No. 5770413
                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
TOPOLOGY: linear MOLECULE TYPE: pro-
FRAGMENT TYPE: int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                     REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                              FILING DATE: 02-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                 TELEFAX: 410
TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                               STRANDEDNESS:
                                                                 TYPE:
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                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0: FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 KYYGYGAGNPLGPAQGYGFANELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 QRLENDLSGYTLTDTEVTYLMDMCSFDTISTSTYDTKLSPFCDLFTHDEWINYDYLQSLK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                         1: 467 amino acids amino acid
                                                                                                                                                                                                               Murashige, Kate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA
                                                                                                                                     415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIJMONS, PETER C.
                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEN, JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOEKEMA, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIETVELD, KRIJN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAN OOIJEN, ALBERT J.J
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              protein
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                                              single
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NAME/KEY: Signal LOCATION: 1...23 OTHER INFORMATION: US-08-693-709-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Patent No. 58
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                               TITLE OF INVENTION: Cloning TITLE OF INVENTION: Phytase 52
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
                                                                                                                                                                                          STREET: 2000 Penr
CITY: Washington
                                   SOFTWARE:
                                                                                                                                                          COUNTRY:
                                                    SOFTWARE:
                                                                                                                                           ZIP: 20006-1888
                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                             D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08419448
                                                                                                                                                                                                               2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                    Petrus A. Van Paridon
Annemarie E. Veenstra
Rudolf G.M. Luttin
                                                                                                                                                                                                                                                                                                                   Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                            Willem Van Hartingsveldt
                                                                                                                                                                                                                                                                                                                                                                                                             Robert F.M. Van Gorcom
                                                                                                                                                              USA
                                                      PatentIn Release #1.0, Version
                                                                                                                                                                                                                             Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.2%; Score 1875; DB 1; 75.6%; Pred. No. 6.3e-188; 75.6%; or mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                    Cloning and Expression of Microbial
   US/08/419,448
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; MOLECULE TYPE: protein US-08-419-448-32
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                                                                                                                                                                                                                                                                 Sequence 3, Application US/08819825 Patent No. 5866118
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-887-1500 INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 10-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGe, Kate H.
REGISTRATION NUMBER: 29,95
REFERENCE/DOCKET NUMBER: 2
                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America,
                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
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COUNTRY: U.S.A. ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLMGQYAPFFSLANE 60
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                                     CITY: New York
STATE: New Yor
                                                                             STREET:
                                                                                               ADDRESSEE:
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                   New York
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                                                                           405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.2%; Score 1875; DB 2; 75.6%; Pred. No. 6.3e-188; ative 41; Mismatches 73;
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COMPUTER READABLE

FORM:

MEDIUM TYPE: COMPUTER: IF

IBM Compatible

Diskette

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                                                                                                                  Sequence 3, Applicatic Patent No. 6221644
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.2%; Score 1875; DB 2; Best Local Similarity 75.6%; Pred. No. 6.3e-188; Matches 353; Conservative 41; Mismatches 73;
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212 867 0298 INFORMATION FOR SEQ ID NO: 3:
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TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
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NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
                                                                                                                                                                                                                                                                                                                       361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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SOFTWARE: FastSE(
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                                                                                                                                                                                                                                                                                                          KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS
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                                                                                                                                                         Application US/09163642
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N: 435
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,867,0123
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ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
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PRIOR APPLICATION DATA:
       421
               421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVBGLSFARSGGNWAECFA 467
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                                                                                                                                                                                                                       241 QRLENDLSGYTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SVISPEVPAGCRYTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120
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STRANDEDNESS: sir
TOPOLOGY: linear
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LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467
                                                                      HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP
                                                                                                         HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                KYYGHGAGNPLGPTQGYGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS
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ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-32/-2951
INFORMATION FOR SEQ ID NO: 32:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                        ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
  301 KYYGYGAGNPLGPAQGYGFANELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                         181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/6
FILING DATE: 24-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/233,510
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                                                                                                                                                                                                                                                                              61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120
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                                         QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300
                                                                                                                      KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240
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                                                                              ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
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Petrus A. Van Paridon
Annemarie E. Veenstra
Rudolf G.M. Luttin
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                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (201) 235-23
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van Loon, Adolphus APPLICANT: Mitchell, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Ca
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NAME/KEY: misc_feature LOCATION: 337
OTHER INFORMATION: /noi
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                                                                                                                                  OTHER INFORMATION:
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                                                                                                NAME/KEY: misc_feature
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                                                                                                                                     /note="potential N-glycosylation site"
 /note="potential N-glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6358722 GENERAL INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Van Loon, Adolphus APPLICANT: Mitchell, David TITLE OF INVENTION: POLYPEPTII
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                            STATE: N
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                                                                                                        FILING DATE:
                                                                                                              APPLICATION NUMBER: US/08/744,231
                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                  Floppy disk
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76.0%; Pred. No. 4.3e-187;
76.0%; Mismatches 74;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                   359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP
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                                                                          361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                             299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS
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REGISTRATION NUMBER:
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  amino acid
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Length 465;
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Дb

В Qy

Qy Дb

Qy

В

419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465

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APPLICANT: KONDO, Hidemasa
APPLICANT: KANEKO, Syunichi
APPLICANT: KANEKO, Syunichi
APPLICANT: KANEKO, Syunichi
APPLICANT: NAGASHIMA, Tadashi
APPLICANT: NAGASHIMA, Tadashi
APPLICANT: NAGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 81356/124
CURRENT APPLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER APPLICATION NUMBER: JP 084314
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-155-855-3
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US-09-155-855-3
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Search completed: July 3, 2002, 09:33:14 Job time: 153 sec
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Patent No. 6139902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 346; Conservative
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                                                                    421 LYRYLYNDRYVPLHGCAYDKLGRCKRDDFYEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                      241 QRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHEEWINYDYLQSLN 300
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                                                                                                                                                                                                                                                                                                          KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
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74.1%; Pred. No. 2.4e-186;
74.1%; Mismatches 73;
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Database: Issued_Patents_AA:*
Database sequences: 231628
Database length: 24425594
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Query Length: 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL-frame+_12p.model -DEV-x1h
-0-/Cgn2_1/USPTO_spool/US09488265/runat_03072002_091241_4286/app_query.fasta_1.4477
-DB=Issued_Patents_AA -OFMT-fastan -SUFFIX=n2p.rai
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-LOOPEXT=0.000 -OGAPOP=4.500 -OGAPEXT=0.050 -YGAPOP=10.000
-YGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pfs -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-GS09488265_@CGN1_1_67 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIIT -THREADS=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
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seq_documentation_block:
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/cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-07-627-539G-2 + 359.00
/cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-07-627-539G-7 + 354.50
/cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-07-923-724-2 + 354.50
/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:US-08-609-426A-2 + 354.50
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APPLICANT: Lebmann, Martin
TITLE OF INVENTION: Consensus Phytases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09121425 Patent No. 6153418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/121,425
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CONSENSUS PHYTASES 13239
CURRENT APPLICATION NUMBER: US/09/121,425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
379 GACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTT
                                                                                                                                                                                                                                                                                                                                 329 AGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC
                                                                                                                                                                                                                                                                                            279 GGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 AATCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 AATTTCTCACTTGTGGGGTACATACTCCTCCATTCTTCTCTTTGGCTGACG
                                                                                                                                                                84 ysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                     34 luSerAlaIleSerProAspValProAspAspCysArgValThrPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 uIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGl
                                       {\tt AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPh}
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97.052
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Percent Identity:
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2.1e-26
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7.4e-27
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1179
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                                                                                                                                                                                                                                                                                                                                                                                                   1029 CTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCT 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheGlnSerAlaLysLeuAlaAspProGlySerGlnProHisGlnAlaSe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCCAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTC 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluLeuSerProPheCysAlaLeuPheThrHisAspGluTrpArgGlnTy
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TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGA 1028
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                                                           AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyAr 417
                                                                                           AACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAG 1328
                                                                                                                                                                                                                                                                                                                                                                    pSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheS 334
                                                                                                                                                       AAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
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1379 GTAACTGGGAAGAATGTTTCGCT 1401

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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-121-425-2
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CURRENT PILING DATE: 198-07-23
EARLIER APPLICATION NUMBER: US/09/121.425
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VEI. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 lyAsnTrpAlaGluCysPheAla 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 TTGACGGTGGTTACCAATGTTTCCCCAGAAATTTCTCACTTGTGGGGTACA 150
                                                                                                                                                                                                                                                     151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
114 snGlnMetValAsnSerGlyIleLysPheTyrArgArgTyrLysAlaLeu
                                     401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
                                                                                                              351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
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Ratio: 5.000
milarity: 89.117
                                                                                             Percent Identity: 85.421
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1241 GTGAAGCTGAAAAGCAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTT 1290
                                                                                                                                                                                                                                                                             1191 TICTIGGACIGTICCATICGCIGCTAGAGCTTACGITGAAATGATGCAAT 1240
                                                                                                                                                                                                                                                                                                                                                                                                                           1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGC 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1091 CTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1041 TACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACA 1090
414 ysGlnAlaGluLysGluProLeuValArgValLeuValAsnAspArgVal 430
                                                                                                                                                                                     381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAl 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 erMetileSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 ProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnProAl 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 laGlnGlyValGlyPheAlaAsnGluLeuIleAlaArgLeuThrArgSer 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCA 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 ysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 uProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              741 GCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGT 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 PheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAspLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 hrCysThrAlaPheGluAspSerGluLeuGlyAspAspValGluAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 TGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAAC 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 sValIleIleProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLy 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGC 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTrpArgGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrCyrAspTyrLeuGlnTyrAspTyrAspTyrLeuGlnTyrAspTyrLeuGlnTyrAspTyrAspTyrLeuGlnTyrAspTyrAspTyrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTATTATTCCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTT 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (201) 235-2363
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                             FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGEN.

ANAME: Kass, Alan P
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TOTAL COLUMN CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1391 AATGTTTCGCT 1401
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Van Loon, APPLICANT: Mitchell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 luCysPheAla 467
                                                                                      OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                                                                                                OTHER INFORMATION: /note="potential N-glycosylation site"
LOCATION:
                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 205
                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 104
OTHER INFORMATION: /note="potential N-glycosylation site"
                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 Kingsland Street
misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Loon, Adolphus
                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/868,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              David
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; NAME/KEY: misc_feature ; LOCATION: 374 ; OTHER INFORMATION: /note="potential N-glycosylation site" US-08-868-435-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 4.506
Percent Similarity: 89.722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-868-435-33 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-488-265-30 x US-08-868-435-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLy 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 TCCAAAGGGTTGTAGAGTTTACTTTCGTTCAAGTTTTTGTCTAGACACACGGTG 250
                                                                                                                                                                                                                                                                                                                            501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
                                                                                                                                                                                                                                                                                                                                                                                                                        451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-744-231-33
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                                                                                                                                                                                                                                                                                                                                                                               1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
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Sequence 33, Application US/08744231 Patent No. 6358722

GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:

ADDRESSEE:

Hoffmann-La Roche Inc

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alignment_block:
US-09-488-265-30 x US-08-744-231-33
                                                                                                                                                                                                                                                                                                                        ; LOCATION: 374; OTHER INFORMATION: /note="potential N-glycosylation site" US-08-744-231-33
                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                Align seg 1/1 to: US-08-744-231-33 from: 1 to: 465
                                                                                                                                                                                                              Percent Similarity:
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INFORMATION FOR SEQ
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     51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
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NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
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APPLICATION NUMBER: 08/4
FILING DATE: 18-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                             1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
                                         1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyAr 17
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/744,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                                                                                                                                                                                Quality: 1888.00
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SYSTEM: PC-DOS/MS-DOS
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201) 235-2363
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951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
                                                                                           299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIl 315
                                                                                                                       901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCCTTCTTGGACT 1200
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                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Production of ITITLE OF INVENTION: in Trichoderma NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
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                PRIOR APPLICATION DATA:
                                       APPLICATION NUMBER: US/07/923,724 FILING DATE: 31-JUL-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                      ZIP: 20005
APPLICATION NUMBER:
                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Fagerstr m, Richard B.
VENTION: Production of Phytase Degrading Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piddington, Christopher S. Rambosek, John A.
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Torkkeli, Tuula K.
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                                                                                                                                                                                                                                                               U.S.A.
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  US 07/496,155
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alignment_block:
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Percent Similarity: 89.079
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 TTGACGGTGGTTACCAATGTTTCCCCAGAAATTTCTCACTTGTGGGGTACA 150
151 ThrArgAsnIleIleProPheIleArgSerSerGlySerSerArgValIl 167
                                                                                                 401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
                                                                                                                                                                                                                                     301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
                                                                                                                                                                                              351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34
                      GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
                                                                                                                                                          sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG
                                                                               InGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150
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1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
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                                                                                         434 isGlyCysProIleAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
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384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
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alignment_block:
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Quality: 1852.00
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US-09-488-265-30 x US-08-609-426A-8
                                                    Percent Similarity:
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GENERAL INFORMATION:
APPLICANT: Nevalation
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          MOLECULE TYPE:
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APPLICANT:
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APPLICATION NUMBER: UK 8
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
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APPLICATION NUMBER: US 0
FILING DATE: 29-APR-1987
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: production of Phytase Degrading Enzymes
NIMPLE OF INVENTION: in Trichoderma
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                                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                 NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/609,426A FILING DATE: 01-MAR-1996
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OPERATING SYSTEM:
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Reed, Grant E.
Reed, Grant E.
P-41,264
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Torkkeli, Tuula K.
Cantrell, Michael
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SYSTEM: PC-DOS/MS-DOS
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Paloheimo, Marja T.
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                                                    89.079
                                                                                                                                                                        protein
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                                                                      4.452
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                                                  Percent Identity:
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                                                                                   Length:
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                                                                                                801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
                                                                                                                                           251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG
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                                                                                                                                                                                                                           hrPheAlaProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyVal
                                                                                                                                                                                                                                                                                                    CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
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                                                                                                                                                                                                                                                                                                                                                                                    ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
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                       TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
                                                        pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284
                                                                                                                                                                                AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
to: US-08-609-426A-8 from: 1
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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-374-652C-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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COMPUTER READABLE FORM:
                                                                                                                                                            CITY: WASHINGTON
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                                                                         COUNTRY:
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                                                                                                                                                                                                                                      ADDRESSEE:
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TURUNEN, MARJA K.
RAMBOSEK, JOHN A.
                                                                                  USA
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CANTRELL, MICHAEL A.
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PALOHEIMO, MARJA T.
FAGERSTROM, RICHARD B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDDINGTON, CHRISTOPHER S.
                                                                                                                                                                                                                                                                                                                                                     RECOMBINANT CELLS, DNA CONSTRUCTS, VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING ENZYMES IN DESIRED RATIOS
                                                                                                                                                                                                                                          KESSLER, GOLDSTEIN & FOX P.L.L.C.
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alignment_block:
US-09-488-265-30 x US-08-374-652C-2
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Ratio: 4.452
Percent Similarity: 89.079
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TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058

FILING DATE: 27-UTL-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/925,401

FILING DATE: 31-UTL-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.

REGISTRATION NUMBER: 41,264

REFERENCE/DOCKET NUMBER: 1050.071001
                                                     351 GACTTACAACTACACTTTGGGTGCTGAACGACTTGACTCCATTCGGTGAAC 400
                                                                                                                                                                                                                                                                              201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTTGTCTAGACACGCGTG 250
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                                                                                                                           67 lProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyA 84
                                                                                                                                                                                                                                                                                                                                                         17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerThrCysAspThrV 34
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
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| 300         | 1201 KAKNOHACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGCTTCCATTGC 1:::  |  |
|-------------|--|--|
| .250<br>.17 | .201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1  |  |
| 1200        | 51 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1  |  |
| 1150<br>384 | CCATTGTCTACTA 1  |  |
| 1100<br>367 | 151 TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC   |  |
| 1050<br>350 | 1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1  |  |
| 1000<br>334 | 951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1   |  |
| 950<br>317  | 01 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT  |  |
| 900<br>300  | STATE   STAT |  |
| 850<br>284  | <pre>i01 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT</pre>  |  |
| 800<br>267  | 51 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA :::  |  |
| 750<br>250  | 01 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT ::   |  |
| 700<br>234  | 51 TTTCGAAGAATCTGAATTGGGTGAACGTTGAAGCTAACTTCACTGCTG  |  |
| 650<br>217  | 01 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC  |  |
| 600<br>200  | 51 ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT  |  |
| 550<br>184  | 01 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG<br>       :::  |  |
| 500<br>167  | 451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT :::   :::   :::   |  |
| 450<br>150  | 401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG   ::::::  |  |
| 134         | 17 sThrTyrAsnTyrSerLeuGlyAlaAspAsp   |  |

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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-151-574-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                    alignment_scores:
                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-151-574-32
                                                   alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32,
Patent No. 5
                                                                                  Percent Similarity:
Align seg 1/1 to: US-08-151-574-32
                                 us-09-488-265-30 \times us-08-151-574-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1401 T 1401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rudolf G.M. Lutt
APPLICANT: Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: _94025-3471
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 24-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       NAME: Murashige, Kate H. REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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P: 545 Middlefield Road,
Menlo Park
                                                                                                                    Quality: 1848.00
                                                                                                                                                                                                                                    amino acids
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                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08151574
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Willem Van Hartingsveldt
Petrus A. Van Paridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1991
                                                                                      4.432
89.293
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                                                                                                                                                                                                                                                                                           32:
                                                                                        Percent Identity: 74.304
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       from: 1
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201 TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 ACCCAGGTGCTAACCCACCAACCTTCTCCAGTTATTAACGTTATTATT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
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                                                                                                                                                                                                                                                                                          217 1PheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaT 234
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901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
                                                                                                                                                                                                                                751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
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                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt SerGluAlaSerSerAsnAsnThrLeuAspProGlyThrCysThrVa}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
                                                                                                                                                                                                                                                                                                                                                                                     TITCGAAGAATCIGAATIGGGIGACGACGTIGAAGCIAACTICACTGCIG 700
                                                                                                                                                                                           ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs 267
                                        euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
                                                                            TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
                                                                                                                 pThrIleSerThrSerThrValAspThrLysLeuSerProPheCysAspL 284
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/08146424 Patent No. 5593963
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
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                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                   TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
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FILING DATE: 02-NOV-1993
CLASSIFICATION: 435
                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      STREET: 755 Page
CITY: Palo Alto
                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                   INVENTION:
                                                                                                                                                                                                                           755 Page Mill Road
                                                                                                                                                                                                                                                                                          SIJMONS, PETER C.
VERWOERD, TEUNIS C.
VENTION: THE EXPRESSION OF PHYTASE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                               VAN OOIJEN, ALBERT J. J. RIETVELD, KRIJN HOEKEMA, ANDREAS
                                                                                                                                                                                                                                                                                                                                                      PEN, JAN
                                                                                                                                                                                                                                               MORRISON & FOERSTER
                             US/08/146,424
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alignment_block:
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; MOLECULE TYPE: protein
US-08-146-424-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-488-265-30 x US-08-146-424-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
551 ACCCAGGTGCTAACCCACACCAAGCTTCTCCCAGTTATTAACGTTATTATT 600
                                                                501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
                                                                                                                                                  151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl
                                                                                                                                                                                            451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT
                                                                                                                                                                                                                                   134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu
                                                                                                                                                                                                                                                                                                                                         351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
                                                                                                                                                                                                                                                                                                                   117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG
                                                                                                                                                                                                                                                                                                                                                                                                   101 GlulleGinGinAsnAlaThrThrPheAspGlyLySTyrAlaPheLeuLy 117
                                                                                                                                                                                                                                                                           401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: KENNEDY, BILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 1848.00
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89.293
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1001 ACCACACTTCTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1101 TATTTTTTTTGGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217
                                                                                               1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
                                                                                                                                                                                                                                                                                                                                                        1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 ThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   701 TTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTT 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1401 T 1401
                                                                                                                                                                                                                                                                                                                                                                                                     401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 spAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhePro 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
467 a 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384
                                                                                                                                                                                                                                                                                                         isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-693-709-2
seq_documentation_block:
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LOCATION: 1...23; OTHER INFORMATION: US-08-693-709-2
                                                                                                                                                                                                                  alignment_block: us-09-488-265-30 \times us-08-693-709-2
                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                   Ratio: 4.432
Percent Similarity: 89.293
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                                                                                                                                                                           Align seg 1/1 to: US-08-693-709-2 from: 1 to: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: FRAGMENT TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: THE EXPRESSION OF PHYTASE TITLE OF INVENTION: IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SIJMONS, PETER C. APPLICANT: VERWOERD, TEUNIS C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02-NOV-1993
ATTORNEY/AGENY INFORMATION:
NAME: MUTAShige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 07-AUG-1996
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: *1-
TELEFAX: 706141
                                 17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34
                                                                   51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
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                                                                                                       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                         Quality: 1848.00
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755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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HOEKEMA, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415-494-0792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                         Percent Identity: 74.304
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                                                                                                                                                                                                                                                                                                           Length:
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1001 ACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCA 1050
                                                                           317 lGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisA 334
                                                                                                                              951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
                                                                                                                                                                                 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyVa
                                                                                                                                                                                                                                 901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
                                                                                                                                                                                                                                                                                  284 euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
                                                                                                                                                                                                                                                                                                                                     851 TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                        801 CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
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250
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seq_documentation_block:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-419-448-32
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGC 1400
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                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Cloning TITLE OF INVENTION: Phytase NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 isGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 450
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 a 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 ArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPheAl 467
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                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 10-APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2000 Peni
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20006-1888
                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08419448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Annemarie E. Veenstra Rudolf G.M. Luttin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Willem Van Hartingsveldt
Petrus A. Van Paridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robert
                                                                                                                                                                                                                                                                                       PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morrison & Foerster
                                                                                                                                                                                            10-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning and Expression of Microbial
                                                                                                                                                                                                                     US/08/419,448
                                                                           24615-20026.10
                                                                                                                                                                                                                                                                                    Version #1.25
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; MOLECULE TYPE: protein US-08-419-448-32
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LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                 151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG 134
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                                                                                                         SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrVa 217
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                                                                                                                                                               CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
                                                                                                                                                                                                                                                                        ACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
                                                                                                                                                                                                                                                                                                                        TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
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Ratio: 4.432
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seq\_documentation\_block:

Sequence 3, Application US/08819825 Patent No. 5866118 GENERAL INFORMATION: APPLICANT: Berka, Randy M.

APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5

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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-819-825-3
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                                                                                                                                           1251 AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
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                                                                                                                                                                                                                                                                                                                                 uGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuH 434
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212 BO .... 3:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE 467 amino acids
                351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                               151 TACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
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TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
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NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 47/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                    34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                             GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG
                                                                        GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117
                                                                                                                                                                                                                              laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
                                                                                                                                                                                                                                                                     TCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTG 250
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Ratio: 4.432
milarity: 89.293
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1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGA 1250
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                                                                                              401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGl
                                                                                                                                                                                        384 hrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
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                                                                                                                                                                                                                   alignment_scores:
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                                                                                                                            alignment_block:
                                                                                                         US-09-488-265-30 x US-09-163-642-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Applica Patent No. 6221644
                                                                      Align seg 1/1 to:
                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 400 STREET: New York CITY: New York TIS.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Berka, Randy M. APPLICANT: Ray, Michael W. APPLICANT: Klotz, Alan V.
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ADDRESSEE: No. 62216440 No. 6221644disk of No. 6221644th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Polypeptides Having Phytase Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/163,642
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                 1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCCGCTTCCAC 50
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                                                                                                                                                                                                                                                                                                                                                LENGTH: 467 amino acids
MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17
                                                                                                                                                                                                  Quality: 1848.00
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451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT
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                                                                                            901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGT 950
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951 TGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAG 1000
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                                                                                                                                         euPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
                                                                                                                                                                                      TGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
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                                                                                                                                                                                                                                                                                     CACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACT 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                              ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICANT:
APPLICANT:
                       CLASSIFICATION: PRIOR APPLICATION DATA:
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                                                                                                           CURRENT APPLICATION DATA:
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ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
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    APPLICATION NUMBER:
                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                   STREET: 545 middlefield Road, Suite 200 CITY: Menlo_Park
                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrT 384
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                                                                                                                                                                                                                                                                                                                   California
                                                                                                                                                                                                                                                                                                USA
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Rudolf G.M. Luttin
07/688,578
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-09-233-510-32 from: 1 to: 467
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INFORMATION FOR SEQ ID NO: 32:
          551 ACCCAGGTGCTAACCCACCCAAGCTTCTCCCAGTTATTAACGTTATTATT 600
                                                  167 eAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLysA 184
                                                                                           501 TGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTG 550
                                                                                                                                                                                                                                                                                                 451 GCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTAT 500
                                                                                                                                                                                                                 134 lnGluLeuValAsnSerGlyIleLysPheTyrGlnArgTyrGluSerLeu 150
                                                                                                                                                                                                                                       401 AACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
                                                                                                                                  151 ThrArgAsnIleValProPheIleArgSerSerGlySerSerArgValIl
                                                                                                                                                                                                                                                                                                                                                                                  101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLy 117
                                                                                                                                                                                                                                                                                                                                                                                                                       301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 TACTCTCCATTCTTCTCTTTTGGCTGACGAATCTGCTATTTCTCCAGACGT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 TTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 laArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu
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LENGTH: 467 amino acids
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NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 TyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerProGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 alAspGlnGlyTyrGlnCysPheSerGluThrSerHisLeuTrpGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 rSerGlyLeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 ATCCGGTACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCAC 50
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REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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89.293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 spProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1151 CTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    651 TTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTG 700
                                                                                                                                                                                                                   1301 ACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTT 1350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      751 AACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGA 800
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                                                                                                                            1351 GAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGGAAGAATGTTTCGC 1400
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467 a 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTA 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSe 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTC 1100
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                                                                                                                                                                                                                                                                                         AAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGC 1300
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-155-855-3
seq_documentation_block:
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; ORGANISM: Aspergillus niger US-09-155-855-3
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Ratio: 4.394
Percent Similarity: 89.722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 3, Application US/09155855
patent No. 6139902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE FILE REFERENCE: 81356/124
CURRENT APPLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEO ID NOS: 7
NUMBER OF SEO ID NOS: 7
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APPLICANT: NAGASHIMA, Tadashi
APPLICANT: TANGE, Tatsuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KONDO, Hidemasa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                         101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLySTyrAlaPheLeuLy 117
                                                                                                                                                                                                                                                                                                                                                                  201
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                                                                                                         401 AACAANTGGTTAACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTG 450
                                                                                                                                                  117 sThrTyrAsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluG
                                                                                                                                                                         351 GACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAC 400
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                         451
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                                                             Percent Identity: 73.233
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| 1251 AAAGGAACCATT  :::         417 uGLnGluPTOLe 1301 ACGGTTGTGGTG          434 isGlyCysProv 1351 GAAGGTTTGTCT :::         451 LysGlyLeuSer | 1051 TTGAACGCTAC;         | 851 TGTTCACTCACG            284 euPheThrHisG 901 AAGTACTACGGT             301 LYSTYTTYTGLY 951 TGGTTTCGTTAA      :::::   111 1317 IGLYTYTALAS 1001 ACCACACTTCTA          334 SPASPThrSerS | 01 TTTTCGCTO<br>::   ::  <br>34 hrPheValp.<br>35 AACTTGACTO<br>:::      <br>51 SerLeuThri<br>51 SerLeuThri<br>51 CACTGTTGC:<br>    :::: | 151 Thrargasn11 501 TGCTTCTGCTG        :::: 167 eAlaSerG1yA 551 ACCCAGGTGCT       184 spProArgAla 601 CCAGAAGGTGC    :::: 201 SerGluAlaSe 651 TTTCGAAGAAT ::     :::: 217 lPheGluAspS; |
|--|---------------------------|---|---|--|
| GGTTAGAGTTTTGGTTAACGACAG/  | TTGTACGCTGACTTCTCTCACGAC! | ACGAATGGATTCAATACGACTACTT ::        :::            !UG1UTPPI1eASNTY/ASPTY/LE TACGGTGCTGGTAACCCATTGGGTC :::  | CCAATTAGAGCTAGATTGGAAGCTCA<br>  | evalProPheIleArgSerSerGly. AAAAGTTCATTGAAGGTTTCCAATC: ::   |
| AGTIGTTCCATTGC 1300  | AACACTATGGTTTC 1100       | GCAATCTTTGGGT 900   | TTGCCAGGTGT   | SerSerArgVall1 16 SCTAAGTTGGCTG 55 ThrLySLeuLysA 16 ThrLySLeuLysA 16 ThrACGTTATTATT 60  :::   ::    :::   ::    :::   ::    ::   ::    ::   ::   |

1401 T 1401 | | 467 a 467

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Result
No.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein -
              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
           1819
1804.5
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                                                                                                        protein search, using sw model
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1: /cgn2_6/ptodata/2,
2: //gn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
           Query
Match
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2468
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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           US-09-121-425-1
US-09-121-425-2
US-08-668-435-3
US-08-744-231-33
US-08-744-231-33
US-08-374-652C-2
US-08-166-424-20
US-08-151-574-32
US-08-16-424-20
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US-08-68-63-53-13
US-09-153-642-3
US-09-153-855-3
US-09-153-855-3
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US-08-868-435-12
US-08-744-231-12
US-08-744-231-12
US-08-744-231-29
US-08-744-231-29
US-09-155-855-2
US-09-155-855-2
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US-09-543-744-2
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288.341 Million cell updates/sec
Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 8, Appli Sequence 8, Appli Sequence 2, Appli Sequence 20, Appli Sequence 20, Appli Sequence 3, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 29, Appli Sequence 29, Appli Sequence 21, Appli Sequence 2, Appli
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| 8 443 3 US-08-993-359-30 8 443 3 US-08-993-359-22 8 Sequence 23 7 439 3 US-08-993-359-24 8 Sequence 24 7 439 3 US-08-993-359-28 9 442 3 US-08-993-359-28 9 442 3 US-08-993-359-28 9 443 1 US-08-993-359-28 9 Sequence 26 1 446 1 US-07-627-539G-2 1 Sequence 26 1 4479 1 US-07-627-539G-7 1 US-07-627-539G-7 2 Sequence 27 1 US-07-627-539G-7 2 Sequence 27 1 US-07-627-539G-7 2 Sequence 27 2 Sequence 28 2 Sequence 28 2 Sequence 29 2 US-08-609-426A-2 2 Sequence 27 2 Sequen | 1.0 466 4 US-08-744-231-2 9.3 466 4 US-08-868-435-31 Sequence 2, 9.3 466 4 US-08-744-231-31 Sequence 31 9.3 466 4 US-08-744-231-31 Sequence 31 6.0 475 2 US-08-819-825-2 Sequence 2, 6.0 475 4 US-08-684-2 Sequence 4, 4.1 487 4 US-08-744-231-4 Sequence 4, 4.3 4 4 3 4 US-08-744-231-4 Sequence 4, |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/121,425
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lehmann, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1997-07-24 NUMBER OF SEQ ID NOS: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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461 NWEECFA 467
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                                                                                                                                                                                                FCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGYGFVNELIARLTHSPYQDHTSTNH 340
                              KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED
                                                                                                                                                                                                                                                                                                                                      KLADPGANPHQASPVIN-------VIIPEGAGYNNTLDHGLCTAFEE 220
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                                                                                                                                                                  FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH
                                                                                                                                                                                                                                   SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280
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                                                                                                  TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT
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pred. No. 1.3e-215;
.1; Mismatches 20;
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US-08-868-435-33
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US-08-868-435-33
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
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                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /note="potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: 119
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                                                                                                                                                                                                                              OTHER INFORMATION: /note="potential N-glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
              LOCATION: 374
OTHER INFORMATION:
                                                                                                      LOCATION:
                                                                                                            NAME/KEY: misc_feature
LOCATION: 337
                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                              NAME/KEY:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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228
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                                                                                                                                                             /note="potential N-glycosylation site"
                  /note="potential N-glycosylation site"
                                                                                      /note="potential N-glycosylation site"
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Best Local Similarity

76.5%;

Score 1888; Pred. No. 1

38; DB 4; 1.7e-186;

Length 465;

Query Match

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                  TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                  REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Cas
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 18-APR-1995
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG
                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Nutley
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                                                                                                                                                                                                                                                                                                                                                                                                                           07110
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: United States of America
465 amino acids
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340 Kingsland Street
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                                    33:
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; OTHER INFORMATION: /note="potential N-glycosylation site" US-08-744-231-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP
                                                                                                           361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                 299 KYYGYGAGNPLGPAQGTGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358
                                                                                                                                                                        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                          239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298
                                                                                                                                                                                                                                                 241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDVLQSLG 300
                                                                                                                                                                                                                                                                                                     180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238
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                                                                                                                                                                                                                                                                                                                                                                                                       121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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hes 359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
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Sequence 8, Application US/07923724, Patent No. 5780292 GENERAL INFORMATION:

APPLICANT:

Nevalainen, Helena K.M

US-07-923-724-8

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                                                                                                                                                                                                                                                                                                                                     Matches
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TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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CLASSIFICATION:
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241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                   181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240
                                                                    181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                                                          121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180
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                                                                                                                                                                                                                                                            1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
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                                                                                                                                                                                   SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                     347;
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Torkkeli, Tuula K.
Cantrell, Michael
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                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 1852; DB 1; Length 467; 74.3%; Pred. No. 9.2e-183;
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; Sequence 8, Application US/08609426A
; Patent No. 5830733
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                                         INFORMATION FOR SEQ ID NO: 8:
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FILING DATE: 19-MAN -
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
APPLICATION NUMBER: 29-APR-1987
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                                                                                       REGISTRATION NUMBER: P-41,2
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                     FILING DATE: 30-APR-1986 ATTORNEY/AGENT INFORMATION:
                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US OF FILING DATE: 19-MAR-1990
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                   APPLICATION NUMBER:
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             467 amino acids
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Houston, Christine S.
VENTION: Production of Phytase Degrading Enzymes
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                                                                                                                                      Grant E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                             APPLICANT: HOUSTON,
APPLICANT: CANTRELL,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                  COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                          STREET: 1100 NEW CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467
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                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 KYYGYGAGNPLGPAQGYGFVNELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                          COUNTRY:
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40. 5834286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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                                                                                                                        USA
                                                                                                                                                                                                                                                                                               CANTRELL,
                                                                                                                                                                                                                                                                                                                                                                            NEVALAINEN, HELENA K.M.
PALOHEIMO, MARJA T.
PAGESTROM, RICHARD B.
MIETTINEN-OINONEN, ARJA S.
                                                                                                                                                                                                                                                                                                          PIDDINGTON, CHRISTOPHER S. HOUSTON, CHRISTINE S.
           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                  RAMBOSEK, JOHN A.
                                                                                                                                                                                                                                                                                                                                                                   TURUNEN, MARJA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                , MICHAEL A.
RECOMBINANT CELLS, DNA CONSTRUCTS,
VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
ENZYMES IN DESIRED RATIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.0%; Score 1852; DB 2; Length 467; 74.3%; Pred. No. 9.2e-183; vative 42; Mismatches 78; Indels
                                                                                                                                                                                   KESSLER, GOLDSTEIN & FOX P.L.L.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467
                                        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                              361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMOCEAEKEP 420
                                                                                                                                                        301 KYYGHGAGNPLGPTQGYGYANELIARLTHSPYHDDTSSNHTLDSNPATFPLNSTLYADFS 360
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TELECOMMUNICATION INFORMATION:
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NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
                                                                                                                                                                                 301 KYYGYGAGNPLGPAQGYGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                      241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300
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                                                                                                                                                                                                                                                                                                                     181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 75.0%; Score 1852; DB 2; Length 467; Local Similarity 74.3%; Pred. No. 9.2e-183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 27-JUI CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 24-MAY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
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                                                                              HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEWNQCQAEQEP
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202-371-2540
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; Sequence 32, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcol
APPLICANT: Willem Van Hartingsve,
APPLICANT: Petrus A. Van Paridon

Robert F.M. Van Gorcom Willem Van Hartingsveldt

Van Paridon

US-08-151-574-32

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; MOLECULE TYPE: protein US-08-151-574-32
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
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TELEPHONE: 415-327-7250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, Kate H.
REGISTRATION NUMBER: 29.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                          181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 246
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  361
                                                                                                             301 KYYGYGAGNPLGPAQGYGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                      241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 74.9%; Score 1848; DB 1; Length 467;
Local Similarity 74.3%; Pred. No. 2.4e-182;
nes 347; Conservative 42; Mismatches 78; Indels
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                                                                                    KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS
                                                                                                                                                                                                                                                                                                 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
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                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: KENNEDY, BILL REGISTRATION NUMBER: 33,407 REFERENCE/DOCKET NUMBER: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                         181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240
                                                                                           181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                                                                                                                  121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 02-NO
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                                                                                                                                                                                                                                                                                                                                                                             74.9%; Score 1848; DB 1; Length 467; Local Similarity 74.3%; Pred. No. 2.4e-182;
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                                                                                                                                                                                                          61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120
                                                                                                                                                                                                                                            61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                  1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
                                                                                                                                                                                                                                                                                                                      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
                                                                                                                                   YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180
                                                                                                                                                                                                                                                                                                                                                               347;
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HOEKEMA, ANDREAS
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                                                                                                                                                                                                                                                                                                                                                               Conservative
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      Best Local Similarity
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                                                                                                                                     MOLECULE TYPE:
FRAGMENT TYPE:
FEATURE:
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 244
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/1.
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                           TELEFAX: 41.
TELFAX: 706141
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                                                                               NAME/KEY: Signal Sequence LOCATION: 1...23 OTHER INFORMATION:
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                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                    STRANDEDNESS:
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STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                        NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
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     74.98;
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 Score 1848; DB 1;
Pred. No. 2.4e-182;
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No.
               Length 467;
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; Sequence 32, 
; Patent No. 5
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TELEPHONE: 202-887-1500 INFORMATION FOR SEQ ID NO:
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                                                         ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,5
REFERENCE/DOCKET NUMBER:
                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                           CLASSIFICATION:
                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 10-APP
                                                                                                                                                                                                                      SOFTWARE:
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                   USA
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Annemarie E. Veenstra
Rudolf G.M. Luttin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Willem Van Hartingsveldt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert F.M. Van Gorcom
                                                                                                                                                                                                                                                                                                                                                                                                                                              Morrison & Foerster
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-419-448-32
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LENGTH: 467 amino acids
                                                                                                                                                                                                                                                 NUMBER OF EXQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Berka, Randy M. APPLICANT: Ray, Michael W. APPLICANT: Klotz, Alan V.
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Polypeptides Having Phytase Activity
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     STREET: 405 Lexi
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
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                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
                                  FILING DATE: 18-MAR-1997
                                                                                                                                  COMPUTER:
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                                                                                                                              IBM Compatible
                                                          US/08/819,825
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; TOPOLOGY: linear US-08-819-825-3
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US-09-163-642-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application Patent No. 6221644
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                                                                                                                                                                                                                  APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62216440 No. 6221644disk of No. 6221644th America,
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REFERENCE/DOCKET NUMBER: 4758.200-US
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                                                           COUNTRY: U.S.A. ZIP: 10174-6401
COMPUTER:
                                                                                                   STATE:
                                                                                                                      CITY: New York
                                                                                                                                      STREET:
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                                                                                                 New York
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                                                                                                                                      405 Lexington Avenue, Suite
IBM Compatible
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RESULT 14
US-09-233-510-32
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                                                                                                           Sequence 32, Application US/09233510 Patent No. 6350602 GENERAL INFORMATION:
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Best Local
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TELEPHANE: 212 867 0123
TELEPAX: 21 867 0298
TELEPAX: 21 867 0298
INFORMATION FOR SEQ ID NO: 3:
                                                     APPLICANT:
APPLICANT:
     APPLICANT:
                       APPLICANT:
                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                  361
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FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/09/163,642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 74.9%; Score 1848; DB 4; Length 467; Local Similarity 74.3%; Pred. No. 2.4e-182; nes 347; Conservative 42; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                        HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP
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                   Willem Van Hartingsveldt
Petrus A. Van Paridon
Annemarie E. Veenstra
Rudolf G.M. Luttin
Gerardus Selten
                                                                                          Robert F.M. Van Gorcom
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FastSEQ for Windows Version 2.0
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acid
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MEDLIM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                361
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Local Similarity 74.3%; Pred. No. 2.4e-182;
hes 347; Conservative 42; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                      61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120
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CITY: Menlo Park
STATE: Californi
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                                                  KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
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421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION, Hidemasa
APPLICANT: KANEKO, Syunichi
APPLICANT: KANEKO, Syunichi
APPLICANT: KANEKO, Syunichi
APPLICANT: TANGE, Tatsuya
ITILE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
ITILE OF TAVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
CURRENT FILING DATE: 1998-10-05
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER APPLICATION NUMBER: JP 084314
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 467
TYPE: PRT
ORGANISM: Aspergillus niger
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Patent No. 6139902
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Best Local Similarity 73.2
Matches 342; Conservative
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Search completed: July 3, 2002, 09:33:16
Job time: 155 sec